



SEQUENCE LISTING

<110> Osteryoung, Katherine W.
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Koksharova, Olga A.
Gao, Hongo

<120> Plastid Division and Related Genes and Proteins, and Methods of Use

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 Pro Ala Val Leu Val Val Gly Gln Gln Thr Asp Gly Lys Ser Ala Leu
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 Val Glu Ala Leu Met Gly Phe Gln Phe Asn His Val Gly Gly Gly Thr
 65 70 75 80
 Lys Thr Arg Arg Pro Ile Thr Leu His Met Lys Tyr Asp Pro Gln Cys
 85 90 95
 Gln Phe Pro Leu Cys His Leu Gly Ser Asp Asp Asp Pro Ser Val Ser
 100 105 110
 Leu Pro Lys Ser Leu Ser Gln Ile Gln Ala Tyr Ile Glu Ala Glu Asn
 115 120 125
 Met Arg Leu Glu Gln Glu Pro Cys Ser Pro Phe Ser Ala Lys Glu Ile
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 Ile Val Lys Val Gln Tyr Lys Tyr Cys Pro Asn Leu Thr Ile Ile Asp
 145 150 155 160
 Thr Pro Gly Leu Ile Ala Pro Ala Pro Gly Leu Lys Asn Arg Ala Leu
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 Gln Val Gln Ala Arg Ala Val Glu Ala Leu Val Arg Ala Lys Met Gln
 180 185 190
 His Lys Glu Phe Ile Ile Leu Cys Leu Glu Asp Ser Ser Asp Trp Ser
 195 200 205
 Ile Ala Thr Thr Arg Arg Ile Val Met Gln Val Asp Pro Glu Leu Ser
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 Arg Thr Ile Val Val Ser Thr Lys Leu Asp Thr Lys Ile Pro Gln Phe
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 Gly Thr Val Val Ala Pro Pro Asp Lys Phe Gly Glu Thr Leu Gln Asp
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 385 390 395 400
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 Gln Tyr His Arg Ala Met Ala Glu Phe Arg Phe Leu Val Gly Ala Ile
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 Gly Glu Ala Ser Thr His Ser Gln Glu Ile Ala Ser Asn Phe Cys Ile

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Met	Arg	Leu	Ala	Asp	Leu	Leu	Asp	Ser	Thr	Leu	Trp	Asn	Arg	Lys	Leu
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Ala	Pro	Ser	Ser	Glu	Arg	Ile	Val	Tyr	Ala	Leu	Val	Gln	Gln	Ile	Phe
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Ser Val Gln His
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35 40 45

Ser Arg Phe Glu Ala Tyr Asn Arg Leu Gln Ala Ala Val Ala Phe
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Gly Glu Lys Leu Pro Ile Pro Glu Ile Val Ala Ile Gly Gly Gln Ser
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Asp Gly Lys Ser Ser Leu Leu Glu Ala Leu Leu Gly Phe Arg Phe Asn
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Val Arg Glu Val Glu Met Gly Thr Arg Arg Pro Leu Ile Leu Gln Met
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Val His Asp Leu Ser Ala Leu Glu Pro Arg Cys Arg Phe Gln Ile Ser
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Arg Ile Phe Phe Val Glu Leu Ala Ile Leu Ile Thr Asp Leu Asp Glu
130 135 140

Asp Ser Glu Glu Tyr Gly Ser Pro Ile Val Ser Ala Thr Ala Val Ala
145 150 155 160

Asp Val Ile Arg Ser Arg Thr Glu Ala Leu Leu Lys Lys Thr Lys Thr
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Ala Val Ser Pro Lys Pro Ile Val Met Arg Ala Glu Tyr Ala His Cys
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Pro Asn Leu Thr Ile Ile Asp Thr Pro Gly Phe Val Leu Lys Ala Lys
 195 200 205

Lys Gly Glu Pro Glu Thr Thr Pro Asp Glu Ile Leu Ser Met Val Lys
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Ser Leu Ala Ser Pro Pro His Arg Ile Leu Leu Phe Leu Gln Gln Ser
 225 230 235 240

Ser Val Glu Trp Cys Ser Ser Leu Trp Leu Asp Ala Val Arg Glu Ile
 245 250 255

Asp Ser Ser Phe Arg Arg Thr Ile Val Val Val Ser Lys Phe Asp Asn
 260 265 270

Arg Leu Lys Glu Phe Ser Asp Arg Gly Glu Val Asp Arg Tyr Leu Ser
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Ala Ser Gly Tyr Leu Gly Glu Asn Thr Arg Pro Tyr Phe Val Ala Leu
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Pro Lys Asp Arg Ser Thr Ile Ser Asn Asp Glu Phe Arg Arg Gln Ile
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Ser Gln Val Asp Thr Glu Val Ile Arg His Leu Arg Glu Gly Val Lys
 325 330 335

Gly Gly Phe Asp Glu Glu Lys Phe Arg Ser Cys Ile Gly Phe Gly Ser
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Ala Pro Ala Thr Leu Ala Leu Leu Glu Glu Arg Cys Ser Glu Val Thr
 370 375 380

Asp Asp Met Leu Arg Met Asp Met Lys Ile Gln Ala Thr Ser Asp Val
 385 390 395 400

Ala His Leu Arg Lys Ala Ala Met Leu Tyr Thr Ala Ser Ile Ser Asn
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His Val Gly Ala Leu Ile Asp Gly Ala Ala Asn Pro Ala Pro Glu Gln
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Trp Gly Lys Thr Thr Glu Glu Glu Arg Gly Glu Ser Gly Ile Gly Ser
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Leu Gln Ala Ala Ala Val Ala Phe Gly Glu Lys Leu Pro Ile Pro Glu		
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 Thr Ala Ala Arg Ser Trp Leu Ala Pro Leu Leu Asp Thr Ala Cys Asp
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-41-

Leu

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gctctagata gttcatccat gccatgt 27

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<400> 85
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<210> 86
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<213> Arabidopsis thaliana

<400> 86

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Val Lys Lys Ala Phe Arg Gln Leu Ala Lys Lys Tyr His Pro Asp Val
 20 25 30

Cys Arg Gly Ser Asn Cys Gly Val Gln Phe Gln Thr Ile Asn Glu Ala
 35 40 45

Tyr Asp Ile Val Leu Lys Gln Ile Lys Asn Gln Met Glu
 50 55 60

<210> 87
 <211> 68
 <212> PRT
 <213> Phaseolus vulgaris

<400> 87

Ser Leu Tyr Asp Ile Leu Gly Ile Pro Ala Gly Ala Ser Ser Gln Glu
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Ile Lys Ala Ala Tyr Arg Arg Leu Ala Arg Val Cys His Pro Asp Val
 20 25 30

Ala Ala Ile Asp Arg Lys Asn Ser Ser Ala Asp Glu Phe Met Lys Ile
 35 40 45

His Ala Ala Tyr Ser Thr Leu Ser Asp Pro Asp Lys Arg Ala Asn Tyr
 50 55 60

Asp Arg Ser Leu
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<210> 88
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 <213> Arabidopsis thaliana

<400> 88

Ser Leu Tyr Glu Ile Leu Glu Ile Pro Val Gly Ser Thr Ser Gln Glu
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Ile Lys Ser Ala Tyr Arg Arg Leu Ala Arg Ile Cys His Pro Asp Val
 20 25 30

Ala Arg Asn Ser Arg Asp Asn Ser Ser Ala Asp Asp Phe Met Lys Ile
 35 40 45

His Ala Ala Tyr Cys Thr Leu Ser Asp Pro Glu Lys Arg Ala Val Tyr
 50 55 60

Asp Arg Arg Thr
65

<210> 89
<211> 63
<212> PRT
<213> *Mycoplasma pneumoniae*

<400> 89

Thr Leu Tyr Asp Leu Leu Glu Leu Pro Gln Thr Ala Thr Leu Gln Glu
1 5 10 15

Ile Lys Thr Ala Tyr Lys Arg Leu Ala Lys Arg Tyr His Pro Asp Ile
20 25 30

Asn Lys Gln Gly Ala Asp Thr Phe Val Lys Ile Asn Asn Ala Tyr Ala
35 40 45

Val Leu Ser Asp Thr Thr Gln Lys Ala Glu Tyr Asp Ala Met Leu
50 55 60

<210> 90
<211> 63
<212> PRT
<213> *Mycoplasma genitalium*

<400> 90

Asn Leu Tyr Asp Leu Leu Glu Leu Pro Thr Thr Ala Ser Ile Lys Glu
1 5 10 15

Ile Lys Ile Ala Tyr Lys Arg Leu Ala Lys Arg Tyr His Pro Asp Val
20 25 30

Asn Lys Leu Gly Ser Gln Thr Phe Val Glu Ile Asn Asn Ala Tyr Ser
35 40 45

Ile Leu Ser Asp Pro Asn Gln Lys Glu Lys Tyr Asp Ser Met Leu
50 55 60

<210> 91
<211> 68
<212> PRT
<213> *Arabidopsis thaliana*

<400> 91

Ser Phe Tyr Asp Leu Leu Gly Val Thr Glu Ser Val Thr Leu Pro Glu
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Ile Lys Gln Ala Tyr Lys Gln Leu Ala Arg Lys Tyr His Pro Asp Val

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55

60

Asn Tyr Asp Tyr Tyr Leu
65 70

<210> 94

<211> 72

<212> PRT

<213> Arabidopsis thaliana

<400> 94

Ser Pro Tyr Asp Thr Leu Glu Leu Asp Arg Asn Ala Glu Glu Glu Gln
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Ile Lys Val Ala Tyr Arg Arg Leu Ala Lys Phe Tyr His Pro Asp Val
20 25 30

Tyr Asp Gly Lys Gly Thr Leu Glu Glu Gly Glu Thr Ala Glu Ala Arg
35 40 45

Phe Ile Lys Ile Gln Ala Ala Tyr Glu Leu Leu Met Asp Ser Glu Lys
50 55 60

Lys Val Gln Tyr Asp Met Asp Asn
65 70

<210> 95

<211> 68

<212> PRT

<213> Schizosaccharomyces pombe

<400> 95

Lys Leu Tyr Asp Ile Leu Glu Val His Phe Glu Ala Ser Ala Glu Glu
1 5 10 15

Ile Lys Lys Ser Tyr Lys Arg Leu Ala Leu Leu His His Pro Asp Lys
20 25 30

Ala Pro Ile His Glu Lys Glu Glu Ala Ala Glu Arg Phe Arg Gly Val
35 40 45

Gln Glu Ala Tyr Asp Ile Leu Lys Asp Pro Glu Ser Arg Glu Met Tyr
50 55 60

Asp Met Tyr Gly
65

<210> 96

<211> 66
<212> PRT
<213> Unknown

<220>
<223> Synthetic

<400> 96

Asp Phe Tyr Lys Ile Leu Gly Ala Glu Pro His Phe Leu Gly Asp Gly
1 5 10 15

Ile Arg Arg Ala Phe Glu Ser Arg Ile Ala Lys Pro Pro Gln Tyr Gly
20 25 30

Tyr Ser Thr Glu Ala Leu Ala Gly Arg Arg Gln Met Leu Gln Ile Ala
35 40 45

His Asp Thr Leu Thr Asn Gln Ser Ser Arg Thr Glu Tyr Asp Arg Ala
50 55 60

Leu Ser
65

<210> 97
<211> 66
<212> PRT
<213> Oryza sativa

<400> 97

Asp Phe Tyr Lys Val Leu Gly Ala Glu Pro His Phe Leu Gly Asp Gly
1 5 10 15

Ile Arg Arg Ala Phe Glu Ala Arg Ile Ala Lys Pro Pro Gln Tyr Gly
20 25 30

Tyr Ser Thr Asp Ala Leu Val Gly Arg Arg Gln Met Leu Gln Ile Ala
35 40 45

His Asp Thr Leu Met Asn Gln Asn Ser Arg Thr Gln Tyr Asp Arg Ala
50 55 60

Leu Ser
65

<210> 98
<211> 66
<212> PRT
<213> Solanum tuberosum

<400> 98

Asp Phe Tyr Arg Val Leu Gly Ala Glu Ala His Phe Leu Gly Asp Gly
1 5 10 15

Ile Arg Arg Cys Tyr Asp Ala Arg Ile Thr Lys Pro Pro Gln Tyr Gly
20 25 30

Tyr Ser Gln Glu Ala Leu Ile Gly Arg Arg Gln Ile Leu Gln Ala Ala
35 40 45

Cys Glu Thr Leu Ala Asp Ser Thr Ser Arg Arg Glu Tyr Asn Gln Gly
50 55 60

Leu Ala
65

<210> 99 -
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 99

Asp Leu Tyr Lys Ile Leu Gly Ala Glu Thr His Phe Leu Gly Asp Gly
1 5 10 15

Ile Arg Arg Ala Tyr Glu Ala Lys Phe Ser Lys Pro Pro Gln Tyr Ala
20 25 30

Phe Ser Asn Glu Ala Leu Ile Ser Arg Arg Gln Ile Leu Gln Ala Ala
35 40 45

Cys Glu Thr Leu Ala Asp Pro Ala Ser Arg Arg Glu Tyr Asn Gln Ser
50 55 60

Leu Val
65

<210> 100
<211> 66
<212> PRT
<213> Arabidopsis thaliana

<400> 100

Asp Phe Tyr Gln Val Leu Gly Ala Gln Thr His Phe Leu Thr Asp Gly
1 5 10 15

Ile Arg Arg Ala Phe Glu Ala Arg Val Ser Lys Pro Pro Gln Phe Gly

50

55

60

Leu Leu
65

<210> 103
<211> 66
<212> PRT
<213> Synechocystis PCC6803

<400> 103

Asp His Phe Arg Leu Leu Gly Val Ser Pro Ser Ala Asp Pro Ala Ser
1 5 10 15

Ile Leu Arg Arg Leu Gln Thr Arg Ser Asp Ser Pro Pro Asp Asp Gly
20 25 30

Phe Thr His Glu Gly Leu Leu Gln Arg Gln Ala Leu Leu His Arg Ser
35 40 45

Ala Asp Leu Leu Thr Asp Pro Ser Glu Arg Ala Asp Tyr Glu Ala Ala
50 55 60

Leu Leu
65

<210> 104
<211> 66
<212> PRT
<213> Synechocystis PCC6803

<400> 104

Asp Phe Tyr Arg Ile Leu Gly Ile Pro Pro Gln Ser Gly Gly Glu Thr
1 5 10 15

Ile Glu Gln Ala Tyr Gln Asp Arg Leu Leu Gln Leu Pro Arg Arg Glu
20 25 30

Phe Ser Asp Ala Ala Val Thr Leu Arg Asn Gln Leu Leu Ala Ile Ala
35 40 45

Tyr Glu Thr Leu Arg Asp Pro Glu Lys Arg Gln Ala Tyr Asp Gln Glu
50 55 60

Trp Trp
65

<210> 105

<211> 66
 <212> PRT
 <213> Nostoc punctiforme

<400> 105

Asp Tyr Tyr Arg Ile Leu Gly Leu Pro Leu Ala Ala Ser Glu Glu Gln
 1 5 10 15

Leu Arg Gln Ala Tyr Ser Asp Arg Ile Val Gln Leu Pro Arg Arg Glu
 20 25 30

Tyr Ser Gln Ala Ala Ile Ser Ser Arg Lys Gln Leu Ile Glu Glu Ala
 35 40 45

Tyr Val Val Leu Ser Asp Pro Lys Gln Arg Ser Thr Tyr Asp Gln Leu
 50 55 60

Tyr Leu
 65

<210> 106
 <211> 66
 <212> PRT
 <213> Anabaena PCC7120

<400> 106

Asp Tyr Tyr Arg Ile Leu Gly Leu Pro Leu Ala Ala Ser Asp Glu Gln
 1 5 10 15

Leu Arg Gln Ala Tyr Ser Asp Arg Ile Val Gln Leu Pro Arg Arg Glu
 20 25 30

Tyr Ser Gln Ala Ala Ile Ala Ser Arg Lys Gln Leu Ile Glu Glu Ala
 35 40 45

Tyr Val Val Leu Ser Asp Pro Lys Glu Arg Ser Ser Tyr Asp Gln Leu
 50 55 60

Tyr Leu
 65

<210> 107
 <211> 66
 <212> PRT
 <213> Bombyx mori

<400> 107

Asp Tyr Tyr Ala Leu Leu Gly Cys Asp Glu Asn Ser Thr Val Glu Gln
 1 5 10 15

Ile Thr Ala Glu Tyr Lys Ile Leu Ala Leu Gln His His Pro Asp Lys
 20 25 30

Asn Asp Gly Glu Lys Glu Ala Glu Met Lys Phe Gln Lys Leu Lys Glu
 35 40 45

Ala Lys Glu Ile Leu Cys Asp Pro Ser Lys Arg Ala Leu Tyr Asp Lys
 50 55 60

Trp Arg
 65

<210> 108

<211> 66

<212> PRT

<213> *Drosophila melanogaster*

<400> 108

Asp Phe Tyr Gly Leu Leu His Cys Asp Glu Asn Ser Ser Pro Glu Gln
 1 5 10 15

Ile Gln Ala Glu Tyr Lys Val Leu Ala Leu Gln Tyr His Pro Asp Lys
 20 25 30

Asn Ser Gly Asp Lys Glu Ala Glu Ala Lys Phe Gln Gln Leu Lys Glu
 35 40 45

Ala Lys Glu Thr Leu Cys Asp Pro Glu Lys Arg Ala Ile Tyr Asp Lys
 50 55 60

Trp Arg
 65

<210> 109

<211> 66

<212> PRT

<213> *Mus musculus*

<400> 109

Asp Tyr Tyr Ala Leu Leu Gly Cys Asp Glu Leu Ser Ser Val Glu Gln
 1 5 10 15

Ile Leu Ala Glu Phe Lys Ile Arg Ala Leu Glu Cys His Pro Asp Lys
 20 25 30

His Pro Glu Asn Ser Lys Ala Val Glu Thr Phe Gln Lys Leu Gln Lys
 35 40 45

Ala Lys Glu Ile Leu Cys Asn Ala Glu Ser Arg Ala Arg Tyr Asp His
50 55 60

Trp Arg
65

<210> 110
<211> 65
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 110

Asp Ala Tyr Ser Ile Leu Gly Val Pro Pro Asp Ser Ser Gln Glu Gln
1 5 10 15

Ile Arg Lys His Tyr Lys Lys Ile Ala Val Leu Val His Pro Asp Lys
20 25 30

Asn Lys Gln Ala Gly Ala Glu Glu Ala Phe Lys Val Leu Gln Arg Ala
35 40 45

Phe Glu Leu Ile Gly Glu Pro Glu Asn Arg Leu Ile Tyr Asp Gln Ser
50 55 60

Ile
65

<210> 111
<211> 64
<212> PRT
<213> *Leishmania major*

<400> 111

Glu Leu Tyr Gln Val Leu Glu Leu Asp Ala Gln Cys Thr Thr Ala Glu
1 5 10 15

Ile Ser Gln Gln Tyr Arg Arg Leu Ala Leu Arg Tyr His Pro Asp Arg
20 25 30

Asn Ala Gly Ala Thr Val Glu Gln Phe Gln Arg Ile Glu Glu Ala His
35 40 45

Arg Val Leu Ser Asp Leu Arg Gln Arg Gln Leu Tyr Asp Thr Val Gly
50 55 60

<210> 112
<211> 67
<212> PRT
<213> *Schizosaccharomyces pombe*

<400> 112

Asp Tyr Tyr Thr Ile Leu Gly Ala Glu Ser Thr Ser Ser Tyr Val Glu
1 5 10 15

Ile Arg Gln Gln Tyr Leu Lys Leu Val Leu Arg Tyr His Pro Asp Arg
20 25 30

Asn Pro Gly Arg Glu Ala Glu Val Leu Pro Gln Phe Gln Leu Ile Gln
35 40 45

Lys Ala His Glu Val Leu Lys Asp Pro Lys Leu Arg Glu Leu Phe Asp
50 55 60

Gln Arg Arg
65

<210> 113

<211> 67

<212> PRT

<213> Schizosaccharomyces pombe

<400> 113

Asp Tyr Tyr Ala Ile Leu Lys Leu Gln Lys Asn Ala Thr Phe Gln Gln
1 5 10 15

Ile Arg Lys Gln Tyr Leu Phe Leu Ala Leu Gln Tyr His Pro Asp Arg
20 25 30

Asn Pro Gly Asp Glu Glu Arg Ala Val Lys Arg Phe Gln Arg Leu Gln
35 40 45

Leu Ala His Glu Val Leu Ser Asp Ala Thr Lys Arg Leu Ile Tyr Asp
50 55 60

Gln Leu Phe
65

<210> 114

<211> 68

<212> PRT

<213> Schizosaccharomyces pombe

<400> 114

Asn His Tyr Ser Val Leu Asn Leu Lys Asp Gly Lys Thr Tyr Thr Asp
1 5 10 15

Asp Glu Ile Lys Glu Ala Tyr Arg Lys Ala Leu Leu Leu Phe His Pro
20 25 30

Asp Lys Cys Lys Glu Lys Pro Ser Val Val Tyr Thr Ile Asp Gln Val
35 40 45

Lys Glu Ala Tyr Gln Val Leu Ser Ser Glu Lys Asp Arg Gln Gln Tyr
50 55 60

Gln Ile Lys Gln
65

<210> 115
<211> 652
<212> PRT
<213> Anabaena PCC7120

<400> 115

Gln Gly Lys Tyr Ala Val Arg Ile Pro Leu Asp Tyr Tyr Arg Ile Leu
1 5 10 15

Gly Leu Pro Leu Ala Ala Ser Asp Glu Gln Leu Arg Gln Ala Tyr Ser
20 25 30

Asp Arg Ile Val Gln Leu Pro Arg Arg Glu Tyr Ser Gln Ala Ala Ile
35 40 45

Ala Ser Arg Lys Gln Leu Ile Glu Glu Ala Tyr Val Val Leu Ser Asp
50 55 60

Pro Lys Glu Arg Ser Ser Tyr Asp Gln Leu Tyr Leu Ala His Ala Tyr
65 70 75 80

Asp Pro Asp Asn Ala Ala Thr Thr Lys Val Ala Val Glu Asn Arg Gly
85 90 95

Asp Ser Asn Asn Gly His Phe Asp Val Gln Ser Leu Ser Ile Glu Val
100 105 110

Ser Ser Glu Glu Leu Ile Gly Ala Leu Leu Ile Leu Gln Glu Leu Gly
115 120 125

Glu Tyr Glu Leu Val Leu Lys Leu Gly Arg Asn Tyr Leu Gly Asn Gln
130 135 140

Asn Gly Thr Ala Ser Thr Arg Asn Gly Asn His Arg Thr Pro Glu Glu
145 150 155 160

Phe Leu Asp Ser Ser Glu Arg Pro Asp Ile Leu Leu Thr Val Ala Leu
165 170 175

Ala Ser Leu Glu Leu Gly Arg Glu Gln Trp Gln Gln Gly His Tyr Glu
180 185 190

Asn Ala Ala Leu Ser Leu Glu Thr Gly Gln Glu Val Leu Phe Ser Glu
195 200 205

Gly Ile Phe Pro Ser Val Gln Ala Glu Ile Gln Ala Asp Leu Tyr Lys
210 215 220

Leu Arg Pro Tyr Arg Ile Leu Glu Leu Leu Ala Leu Pro Gln Glu Lys
225 230 235 240

Thr Ile Glu Arg His Gln Gly Leu Asp Leu Leu Gln Ser Ile Leu Asp
245 250 255

Asp Arg Gly Gly Ile Asp Gly Thr Gly Asn Asp Gln Ser Gly Leu Asn
260 265 270

Ile Asp Asp Phe Leu Arg Phe Ile Gln Gln Leu Arg His His Leu Thr
275 280 285

Val Ala Glu Gln His Lys Leu Phe Asp Gly Glu Ser Lys Arg Pro Ser
290 295 300

Ala Val Ala Thr Tyr Leu Ala Val Tyr Ala Ser Ile Ala Arg Gly Phe
305 310 315 320

Thr Gln Arg Gln Pro Ala Leu Ile Arg His Ala Lys Gln Ile Leu Met
325 330 335

Arg Leu Ser Lys Arg Gln Asp Val His Leu Glu Gln Ser Leu Cys Ala
340 345 350

Leu Leu Leu Gly Gln Thr Glu Glu Ala Thr Arg Val Leu Glu Leu Ser
355 360 365

Gln Glu Tyr Glu Ala Leu Ala Leu Ile Arg Glu Lys Ser Gln Asp Ser
370 375 380

Pro Asp Leu Leu Pro Gly Leu Cys Leu Tyr Ala Glu Gln Trp Leu Gln
385 390 395 400

Asn Glu Val Phe Pro His Phe Arg Asp Leu Ser Arg Gln Gln Ala Ser
405 410 415

Leu Lys Asp Tyr Phe Ala Asn Gln Gln Val Gln Ala Tyr Leu Glu Ala

420	425	430
Leu Pro Asn Asp Ala Glu Thr Thr Asn Glu Trp Ala Val Ile Asn Arg 435 440 445		
Gln Ser Phe Ser Gln Pro Arg Gly Asn Ser Tyr Ser Gly Gly Thr Pro 450 455 460		
Val Ala Lys Arg Pro Val Gly Lys Ala Asn Arg Pro Gly Glu Ala Ser 465 470 475 480		
Thr Arg Pro Val Pro Gln Arg Ser His Pro Ser Glu Val Asn Arg Gln 485 490 495		
Phe His Gln Asn Arg Thr Pro Asp Pro Glu Leu Pro Glu Thr Ser Asn 500 505 510		
His Arg Arg Pro Glu Ser Ser Asn Phe Thr Thr Ala Arg Glu Asn Ile 515 520 525		
Ser Thr Thr Asp Ala Tyr Thr Asp Asn Tyr Pro Pro Glu Ile Pro Val 530 535 540		
Glu Arg Ala Ser Arg Pro Val Gln Pro Gly Val Ser Gly Tyr Thr Gln 545 550 555 560		
Ser Thr Pro Pro Arg Gln Thr Pro Lys Arg Arg Arg Arg Lys Lys Pro 565 570 575		
Gln Ala Val Val Asn Arg Gly His Ser Ile His Gln Gln Arg Gln Pro 580 585 590		
Ser Pro Ser Thr Leu Gly Arg Lys Thr Arg Leu Leu Trp Ile Val Leu 595 600 605		
Gly Ser Leu Gly Gly Ile Leu Leu Phe Trp Leu Ile Val Ser Thr Thr 610 615 620		
Phe Gly Trp Leu Lys Asn Val Phe Phe Pro Ala Pro Ser Leu Gln Gly 625 630 635 640		
Glu Gln Leu Ser Ile Gln Ile Ser Gln Pro Pro Leu 645 650		
<210> 116		
<211> 624		
<212> PRT		

<213> Nostoc punctiforme

<400> 116

Met Arg Ile Pro Leu Asp Tyr Tyr Arg Ile Leu Gly Leu Pro Leu Ala
1 5 10 15

Ala Ser Glu Glu Gln Leu Arg Gln Ala Tyr Ser Asp Arg Ile Val Gln
20 25 30

Leu Pro Arg Arg Glu Tyr Ser Gln Ala Ala Ile Ser Ser Arg Lys Gln
35 40 45

Leu Ile Glu Glu Ala Tyr Val Val Leu Ser Asp Pro Lys Gln Arg Ser
50 55 60

Thr Tyr Asp Gln Leu Tyr Leu Ala His Ala Tyr Asp Pro Asp Asn Leu
65 70 75 80

Ala Ala Ala Ala Val Ala Gln Glu Asn Arg Thr Glu Ser Thr Lys Arg
85 90 95

Gly Ser Asp Thr Gln Ser Leu Gly Ile Glu Ile Thr Gln Asp Glu Leu
100 105 110

Val Gly Ala Leu Leu Ile Leu Gln Glu Leu Gly Glu Tyr Glu Leu Val
115 120 125

Leu Lys Leu Gly Arg Pro Tyr Leu Val Asn Lys Asn Ser Ala Thr Ser
130 135 140

Ser Arg Lys Ser Asn Asn Leu Ala Asp Glu Glu Ile Tyr Glu Ser Ala
145 150 155 160

Glu His Pro Asp Val Val Leu Thr Val Ala Leu Ala Cys Leu Glu Leu
165 170 175

Gly Arg Glu Gln Trp Gln Gln Gly His Tyr Glu Asn Ala Ala Ile Ser
180 185 190

Leu Glu Thr Gly Gln Glu Leu Leu Val Arg Glu Gly Leu Phe Ser Ser
195 200 205

Ile Gln Ala Glu Ile Gln Ala Asp Leu Tyr Lys Leu Arg Pro Tyr Arg
210 215 220

Ile Leu Glu Leu Leu Ala Leu Pro Gln Glu Lys Thr Ala Glu Arg Ser
225 230 235 240

Gln Gly Leu Glu Leu Leu Gln Asn Leu Leu Glu Asp Arg Gly Gly Ile
245 250 255

Asp Gly Thr Asn Asn Asp Glu Ser Gly Leu Asn Ile Asp Asp Phe Leu
260 265 270

Arg Phe Ile Gln Gln Leu Arg Asn His Leu Thr Val Ala Glu Gln His
275 280 285

Lys Leu Phe Glu Ala Gln Ser Lys Arg Ser Ser Ala Val Ala Thr Tyr
290 295 300

Leu Ala Val Tyr Ala Leu Ile Ala Arg Gly Phe Ala Gln Arg Gln Pro
305 310 315 320

Ala Leu Ile Arg Gln Ala Arg Gln Met Leu Val Arg Leu Gly Lys Arg
325 330 335

Gln Asp Val His Leu Glu Gln Ser Leu Cys Ala Leu Leu Leu Gly Gln
340 345 350

Thr Glu Glu Ala Thr Arg Val Leu Glu Leu Ser Gln Glu Tyr Glu Ala
355 360 365

Leu Ala Phe Ile Arg Glu Lys Ser Gln Asp Ser Pro Asp Leu Leu Pro
370 375 380

Gly Leu Cys Leu Tyr Ala Glu Gln Trp Leu Gln His Glu Val Phe Pro
385 390 395 400

His Phe Arg Asp Leu Ala Asn Gln Gln Ala Phe Leu Lys Asp Tyr Phe
405 410 415

Ala Asn Gln Gln Val Gln Ala Tyr Leu Glu Ala Leu Pro Thr Asp Ala
420 425 430

Gln Thr Thr Asn Glu Trp Ala Val Ile Asn Pro Gln Tyr Phe Pro Gln
435 440 445

Ala Lys Ala Lys Asn Thr His Phe His Asn Asn Ser Thr Lys Thr Ser
450 455 460

Ala Ser Phe Asn His Ser Arg Val Pro Asn Pro Asp Leu Pro Glu Thr
465 470 475 480

Pro Thr Lys Glu Thr Ser Glu Tyr Pro Asn Phe Ser Pro Pro Met Trp

Ser Asn Arg Glu Val Ala Gly Leu Ile Leu Leu Trp Glu Ser Gly Ser
85 90 95

Ser Lys Glu Ala Phe Lys Ile Thr Arg Lys Ala Leu Gln Pro Pro Gln
100 105 110

Thr Pro Ala Leu Gly Ser Ser Arg Glu Ala Asp Leu Thr Leu Leu Ala
115 120 125

Ala Leu Thr Ser Arg Asp Ala Ala Ile Gln Glu Gln Asp Gln Arg Ser
130 135 140

Tyr Ser Asn Ala Ala Asp Phe Leu Gln Glu Gly Ile Gln Leu Leu Gln
145 150 155 160

Arg Met Gly Lys Leu Gly Glu Leu Arg Lys Thr Leu Glu Glu Asp Leu
165 170 175

Val Ser Leu Leu Pro Tyr Arg Ile Leu Asp Leu Leu Ser Arg Asp Leu
180 185 190

Asn Asp Tyr Asp Ser His Lys Lys Gly Leu Ser Met Leu Glu Asn Leu
195 200 205

Ile Ile Lys Arg Gly Gly Leu Glu Gly Lys Asn Lys Ser Glu Tyr Asn
210 215 220

Asp Phe Leu Asn Gln Gln Glu Phe Glu Ser Phe Phe Gln Gln Ile Lys
225 230 235 240

Pro Phe Leu Thr Val Gln Asp Gln Ile Asp Leu Phe Leu Glu Leu Gln
245 250 255

Lys Arg Gly Ser Ser Glu Ala Gly Phe Leu Ala Phe Leu Ser Leu Thr
260 265 270

Ala Ile Gly Phe Ala Arg Arg Lys Pro Ala Lys Leu Phe Glu Ala Arg
275 280 285

Lys Ile Leu Lys Lys Leu Asn Leu Ser Gly Leu Asp Ser Met Pro Leu
290 295 300

Ile Gly Cys Leu Asp Leu Leu Leu Ala Asp Val Glu Gln Ser Ser Ala
305 310 315 320

Arg Phe Leu Ser Ser Ser Asp Glu Lys Leu Arg Asp Trp Leu Asn Asn
325 330 335

Tyr Pro Gly Glu Lys Leu Glu Ala Ile Cys Ile Phe Cys Lys Asn Trp
340 345 350

Leu Glu Asn Asp Val Leu Val Gly Tyr Arg Asp Ile Asp Leu Lys Glu
355 360 365

Ile Asp Leu Asp Ser Trp Phe Glu Asp Arg Glu Ile Gln Glu Phe Ile
370 375 380

Glu Gln Ile Glu Lys Lys Ser Asn Arg Thr Val Phe Lys Ser Gly Pro
385 390 395 400

Gln Asn Lys Pro Ile Phe Gln Ala Gln Glu Ser Leu Lys Asp Ser Ser
405 410 415

Thr Gly Pro Asp Leu Asn Ser Asp Asn Phe Glu Glu Gly Arg Leu Pro
420 425 430

Leu Pro Gly Gly Val Arg Glu Asp Gly Gln Glu Val Ile Glu Glu Asn
435 440 445

Ile Tyr Thr Asp Glu Ile Ile Lys Asn Lys Ser Ile Glu Phe Tyr Lys
450 455 460

Tyr Ala Ile Glu Lys Ile Ala Glu Leu Lys Phe Val Phe Gly Glu Ala
465 470 475 480

Leu Glu Asn Tyr Arg Ile Phe Asn Lys Ser Ser Tyr Leu Thr Tyr Leu
485 490 495

Tyr Ala Phe Leu Ile Leu Phe Ala Phe Gly Leu Gly Val Gly Phe Val
500 505 510

Arg Asn Asn Leu Lys Lys Pro Val Gln Glu Lys Glu Ile Ile Asp Asn
515 520 525

Ser Leu Ser Ile Asn Glu Asn Lys Asn Val Phe Tyr Glu Gly Leu Asn
530 535 540

Gln Asp Asp Lys Lys Lys Val Leu Asp Asn Ser Lys Ile
545 550 555

<210> 118
<211> 524
<212> PRT
<213> Protochlorococcus marinus MT9313

<400> 118

Met Ala Ala Gln Leu Val Asp Leu Pro Ile Asp His Phe Arg Leu Leu
1 5 10 15

Gly Val Ser Pro Ser Ala Asp Ser Glu Ala Ile Leu Arg Ala Leu Glu
20 25 30

Leu Arg Leu Asp Arg Cys Pro Asp Gln Gly Phe Thr His Glu Val Leu
35 40 45

Ile Gln Arg Ala Glu Leu Leu Arg Leu Ser Ala Asp Leu Leu Thr Asp
50 55 60

Pro Pro Arg Arg Gln Ala Tyr Glu Thr Ala Leu Leu Glu Leu Ser Arg
65 70 75 80

Asp His Pro Gly Glu Thr Ala Gly Leu Asp Val Ser Pro Ser Arg Glu
85 90 95

Val Ala Gly Leu Ile Leu Leu Phe Glu Ala Asn Ser Ser His Glu Val
100 105 110

Phe His Leu Ala Ser Gln Gly Leu Gln Pro Pro Gln Ser Pro Thr Leu
115 120 125

Gly Ser Glu Arg Glu Ala Asp Leu Ala Leu Leu Ala Leu Ala Cys
130 135 140

Arg Ala Ala Ala Ala Glu Glu Gln Glu Gln Arg Arg Tyr Glu Ala Ala
145 150 155 160

Ala Ser Leu Leu His Asp Gly Ile Gln Leu Leu Gln Arg Met Gly Lys
165 170 175

Leu Ser Glu Glu Cys His Lys Leu Glu Asn Asp Leu Asp Ala Leu Leu
180 185 190

Pro Tyr Arg Ile Leu Asp Leu Leu Ser Arg Asp Leu Gly Asp Gln Val
195 200 205

Ser His Gln Glu Gly Leu Arg Leu Leu Asp Asn Phe Val Ser Gln Arg
210 215 220

Gly Gly Leu Glu Gly Thr Ala Pro Ser Pro Ala Pro Gly Gly Leu Asp
225 230 235 240

Gln Ser Glu Phe Asp Asn Phe Phe Lys Gln Ile Arg Lys Phe Leu Thr
 245 250 255
 Val Gln Glu Gln Val Asp Leu Phe Leu Arg Trp Gln Gln Ala Gly Ser
 260 265 270
 Ala Asp Ala Gly Phe Leu Gly Gly Leu Ala Leu Ala Ala Val Gly Phe
 275 280 285
 Ser Arg Arg Lys Pro Glu Arg Val Gln Glu Ala Arg Gln His Leu Glu
 290 295 300
 Arg Leu Gln Leu Asp Gly Cys Asp Pro Leu Pro Met Leu Gly Cys Leu
 305 310 315 320
 Asp Leu Leu Leu Gly Asp Val Gly Arg Ala Gln Glu Arg Phe Leu Arg
 325 330 335
 Ser Thr Asp Pro Arg Val Lys Asp Cys Leu Asn Ser His Pro Gly Asp
 340 345 350
 Glu Leu Ala Ala Phe Cys Glu Tyr Cys Arg Ser Trp Leu Arg Gly Asp
 355 360 365
 Val Leu Pro Gly Tyr Arg Asp Val Asp Ala Glu Ala Val Asp Leu Glu
 370 375 380
 Ala Trp Phe Ala Asp Arg Asp Val Gln Ala Tyr Val Glu Arg Leu Glu
 385 390 395 400
 Arg Ser Glu Asn Arg Ala Ser Ser Leu Gly Lys Ala Phe Ser Gly Ser
 405 410 415
 Ser Val Lys Gln Pro Phe Pro Trp Ala Pro Leu Asp Pro Asp Gly Ile
 420 425 430
 Leu Pro Leu Ser Leu Gly Gly Pro Asp Val Gly Gln Pro Ala Ala Asp
 435 440 445
 Gln Ser Ser Asp Glu Phe Ala Ser Asp Gly Met Ala Trp Ile Asp Arg
 450 455 460
 Leu Ala Asp Leu Pro Arg Pro Thr Arg Pro Val Leu Ile Gly Ser Val
 465 470 475 480
 Val Phe Ala Ala Leu Ile Ala Ala Phe Ala Gly Phe Ser Leu Phe Gly
 485 490 495

Gln Arg Pro Arg Thr Ser Val Ser Thr Ala Ala Asp Gln Pro Gln Val
500 505 510

Thr Ala Pro Pro Thr Ala Thr Leu Gln Glu Glu Val
515 520

<210> 119
<211> 566
<212> PRT
<213> Synechocystis PCC6803

<400> 119

Met Phe Ile Pro Leu Asp Phe Tyr Arg Ile Leu Gly Ile Pro Pro Gln
1 5 10 15

Ser Gly Gly Glu Thr Ile Glu Gln Ala Tyr Gln Asp Arg Leu Leu Gln
20 25 30

Leu Pro Arg Arg Glu Phe Ser Asp Ala Ala Val Thr Leu Arg Asn Gln
35 40 45

Leu Leu Ala Ile Ala Tyr Glu Thr Leu Arg Asp Pro Glu Lys Arg Gln
50 55 60

Ala Tyr Asp Gln Glu Trp Trp Gly Ala Met Asp Glu Ala Leu Gly Glu
65 70 75 80

Ala Leu Pro Leu Thr Thr Pro Glu Leu Glu Cys Ser Pro Glu Gln Glu
85 90 95

Ile Gly Ala Leu Leu Ile Leu Leu Asp Leu Gly Glu Tyr Glu Leu Val
100 105 110

Val Lys Tyr Gly Glu Pro Val Leu His Asp Pro Asn Pro Pro Ala Gly
115 120 125

Gly Leu Pro Gln Asp Tyr Leu Leu Ser Val Ile Leu Ala His Trp Glu
130 135 140

Leu Ser Arg Glu Arg Trp Gln Gln Gln Gln Tyr Glu Phe Ala Ala Thr
145 150 155 160

Ala Ser Leu Lys Ala Leu Ala Arg Leu Gln Gln Asp Asn Asp Phe Pro
165 170 175

Ala Leu Glu Ala Glu Ile Arg Gln Glu Leu Tyr Arg Leu Arg Pro Tyr
180 185 190

Arg Ile Leu Glu Leu Leu Ala Lys Glu Gly Gln Gly Glu Glu Gln Arg
195 200 205

Gln Gln Gly Leu Ala Leu Leu Gln Ala Met Val Gln Asp Arg Gly Gly
210 215 220

Ile Glu Gly Lys Gly Glu Asp Tyr Ser Gly Leu Gly Asn Asp Asp Phe
225 230 235 240

Leu Lys Phe Ile His Gln Leu Arg Cys His Leu Thr Val Ala Glu Gln
245 250 255

Asn Ala Leu Phe Leu Pro Glu Ser Gln Arg Pro Ser Leu Val Ala Ser
260 265 270

Tyr Leu Ala Val His Ser Leu Met Ala Glu Gly Val Lys Glu Gln Asp
275 280 285

Pro Met Ala Ile Val Glu Ala Lys Ser Leu Ile Ile Gln Leu Glu Asn
290 295 300

Cys Gln Asp Leu Ala Leu Glu Lys Val Ile Cys Glu Leu Leu Leu Gly
305 310 315 320

Gln Thr Glu Val Val Leu Ala Ala Ile Asp Gln Gly Asp Pro Lys Ile
325 330 335

Val Ala Gly Leu Glu Ser Lys Leu Ala Thr Gly Glu Asp Pro Leu Thr
340 345 350

Ala Phe Tyr Thr Phe Thr Glu Gln Trp Leu Glu Glu Glu Ile Val Pro
355 360 365

Tyr Phe Arg Asp Leu Ser Pro Glu Thr Leu Ser Pro Lys Ala Tyr Phe
370 375 380

Asn Asn Pro Ser Val Gln Gln Tyr Leu Glu Gln Leu Glu Pro Asp Ser
385 390 395 400

Phe Thr Thr Asp Asn Ser Phe Ala Ser Pro Ala Leu Leu Ser Thr Ala
405 410 415

Thr Glu Ser Glu Thr Pro Met Val His Ser Ser Ala Ala Leu Pro Asp
420 425 430

Arg Pro Leu Thr Ser Thr Val Pro Ser Arg Arg Gly Arg Ser Pro Arg

435	440	445
Arg Ser Arg Asp Asp Val Phe Pro Ser Ala Asp Asn Ser Ser Gly Leu 450 455 460		
Ala Val Thr Thr Leu Ser Pro Ala Ile Ala Tyr Asp Thr His Ser Leu 465 470 475 480		
Gly Thr Asn Gly Ile Gly Gly Asp Ser Thr Ser Asn Gly Phe Ser Ser 485 490 495		
Asn Ser Ala Pro Glu Ser Thr Ser Lys His Lys Ser Pro Arg Arg Arg 500 505 510		
Lys Lys Arg Val Thr Ile Lys Pro Val Arg Phe Gly Ile Phe Leu Leu 515 520 525		
Cys Leu Ala Gly Ile Val Gly Gly Ala Thr Ala Leu Ile Ile Asn Arg 530 535 540		
Thr Gly Asp Pro Leu Gly Gly Leu Leu Glu Asp Pro Leu Asp Val Phe 545 550 555 560		
Leu Asp Gln Pro Ser Glu 565		
<210> 120		
<211> 573		
<212> PRT		
<213> Synechococcus PCC7002		
<400> 120		
Thr Val Arg Ile Pro Leu Asp Tyr Tyr Arg Ile Leu Cys Val Pro Ala 1 5 10 15		
Lys Ala Thr Thr Ala Gln Ile Thr Gln Ala Tyr Arg Asp Arg Leu Ser 20 25 30		
Gln Phe Pro Arg Arg Glu His Asn Ala Leu Ala Ile Glu Ala Arg Asn 35 40 45		
Arg Ile Ile Glu Gln Ala Phe Glu Val Leu Ser Gln Thr Glu Thr Arg 50 55 60		
Ala Val Tyr Asp His Glu Leu Ser Gly Asn Met Phe Arg Ser Leu Val 65 70 75 80		

Pro Ser Arg Pro Lys Leu Pro Phe Pro Asp Arg Pro Ser Ser Asp Thr
 85 90 95
 Glu Leu Glu Ala Leu Thr Ala His Gln Pro Thr Ile Asp Ile Ala Glu
 100 105 110
 Lys Asp Leu Leu Gly Gly Leu Leu Leu Leu Asp Leu Gly Glu Tyr
 115 120 125
 Glu Leu Val Leu Lys Trp Ala Ala Pro Tyr Leu Lys Gly Lys Gly Lys
 130 135 140
 Leu Val Lys Glu Gly Lys Phe Gly Ala Val Glu Ile Val Glu Gln Glu
 145 150 155 160
 Leu Arg Leu Cys Leu Ala Leu Ala His Trp Glu Leu Ser Arg Glu Gln
 165 170 175
 Trp Leu Gln Gln His Tyr Glu Gln Ala Ala Leu Ser Gly Gln Lys Ser
 180 185 190
 Gln Glu Leu Leu Val Asp Val Ala Gln Phe Ala Asp Leu Gln Gln Glu
 195 200 205
 Ile Gln Gly Asp Leu Asn Arg Leu Arg Pro Tyr Gln Val Leu Glu Leu
 210 215 220
 Leu Ala Leu Pro Glu Ser Glu Thr Gln Glu Arg Gln Arg Gly Leu Gln
 225 230 235 240
 Leu Leu Gln Glu Met Leu Ser Ala Arg Val Gly Ile Asp Gly Gln Gly
 245 250 255
 Asp Asp Gln Ser Gly Leu Ser Ile Asp Asp Phe Leu Arg Phe Ile Gln
 260 265 270
 Gln Leu Arg Ser Tyr Leu Thr Val Gln Glu Gln Leu Asp Leu Phe Val
 275 280 285
 Ala Glu Ser Lys Arg Pro Ser Ala Ala Ala Ala Tyr Leu Ala Val Tyr
 290 295 300
 Ala Leu Leu Ala Ala Gly Phe Ser Gln Arg Lys Pro Asp Leu Val Val
 305 310 315 320
 Gln Ala Gln Thr Leu Leu Lys Arg Leu Gly Lys Arg Gln Asp Val Phe
 325 330 335

Leu Glu Gln Ser Ile Cys Ala Leu Leu Leu Gly Gln Pro Ser Glu Ala
340 345 350

Asn Gln Leu Leu Glu Gln Ser Gln Glu Gln Glu Ala Ile Ala Tyr Ile
355 360 365

Gln Glu Gln Ser Glu Gly Ala Pro Asp Leu Leu Pro Gly Leu Cys Leu
370 375 380

Tyr Gly Glu Gln Trp Leu Lys Thr Glu Val Phe Ser His Phe Arg Asp
385 390 395 400

Leu Arg Gln Arg Leu Glu Asp Gly Ser Val Ser Leu Thr Ala Tyr Phe
405 410 415

Ala Asp Pro Glu Val Gln Gln Tyr Leu Asp Asp Leu Leu Thr Glu Ala
420 425 430

Val Pro Thr Pro Thr Pro His Pro Asp Thr Glu Ser Thr Ala Ala Pro
435 440 445

Ser Glu Lys Pro Pro Glu Thr Leu Gln Ser Glu Thr Gly Val Ser Pro
450 455 460

His Pro Ser Arg Pro Ala Lys Val Asp Ser Phe Glu Asp Leu Val Thr
465 470 475 480

Gln Thr Pro Ala Thr Val Pro Pro Ala Pro Pro Ser Pro Gly Val Ala
485 490 495

Pro Val Thr Ala Ala Leu Asn Pro Asp Pro Glu Ala Ser Ser Ala Ser
500 505 510

Ser Lys Ser Val Ser Ser Lys Lys Ser Ile Gly Pro Trp Gly Ala Ile
515 520 525

Ala Ala Ile Val Gly Ser Val Leu Leu Val Val Gly Leu Val Arg Ile
530 535 540

Leu Ser Gly Leu Thr Thr Gln Glu Pro Leu Gln Val Thr Leu Asn Gly
545 550 555 560

Glu Pro Pro Leu Thr Ile Pro Ser Leu Asp Thr Ala Glu
565 570

<210> 121

<211> 515
 <212> PRT
 <213> Synechococcus WH8102

<400> 121

Gly Asp Leu Trp Thr Leu Asp Leu Pro Ile Asp His Phe Arg Leu Leu
 1 5 10 15

Gly Val Ser Pro Ser Ala Asp Pro Ala Ser Ile Leu Arg Arg Leu Gln
 20 25 30

Thr Arg Ser Asp Ser Pro Pro Asp Asp Gly Phe Thr His Glu Gly Leu
 35 40 45

Leu Gln Arg Gln Ala Leu Leu His Arg Ser Ala Asp Leu Leu Thr Asp
 50 55 60

Pro Ser Glu Arg Ala Asp Tyr Glu Ala Ala Leu Leu Ser Leu Ser Ala
 65 70 75 80

Thr His Pro Asn Glu Thr Val Gly Leu Asp Leu Ala Ala Ser Ser Glu
 85 90 95

Val Ala Gly Leu Ile Leu Leu Trp Glu Ala Gly Ala Ala Leu Glu Ala
 100 105 110

Phe Gln Leu Ala Arg Gln Gly Leu Gln Pro Pro Gln Ala Pro Ala Leu
 115 120 125

Gly Ser Gly Arg Glu Ala Asp Leu Thr Leu Leu Ala Ala Leu Ala Cys
 130 135 140

Arg Asp Ala Ala Arg Asp Glu Gln Gln Gln Arg Arg Tyr Glu Ser Ala
 145 150 155 160

Ala Gln Leu Leu Arg Asp Gly Ile Glu Leu Gln Gln Arg Met Gly Lys
 165 170 175

Leu Pro Asp Gln Gln Ala Arg Leu Gln Gln Glu Leu Asp Asp Leu Leu
 180 185 190

Pro Tyr Arg Val Leu Asp Leu Leu Ser Arg Asp Leu Ser Asp Ala Asp
 195 200 205

Ala Arg Gln Gln Gly Ile Ser Leu Leu Asp Gln Leu Val Arg Asp Arg
 210 215 220

Gly Gly Leu Asp Pro Glu Gly Leu Asp Ser Glu Thr Pro Ala Ala Met
 225 230 235 240

Gly Gln Ala Asp Phe Glu Ser Phe Phe Gln Gln Ile Arg Arg Phe Leu
 245 250 255

Thr Val Gln Glu Gln Val Asp Leu Phe Arg Gly Trp Phe Ala Glu Gly
 260 265 270

Ser Ile Glu Ala Gly Cys Leu Ala Val Phe Ala Leu Ala Ala Ala Gly
 275 280 285

Tyr Ser Arg Arg Lys Pro Glu Phe Leu Glu Gln Ala Arg Glu Gln Leu
 290 295 300

Gln Arg Leu Val Ala Ser Asp Leu Asp Pro Met Pro Leu Leu Gly Cys
 305 310 315 320

Leu Asp Leu Leu Leu Gly Asn Val Ala Glu Ala Ser Leu His Phe Ser
 325 330 335

Ala Ile Arg Asp Glu Glu Leu Leu Ser Trp Leu Ala Glu His Pro Gly
 340 345 350

Asp His Leu Ala Ala Gln Cys Glu Tyr Cys Arg Val Trp Leu Glu Arg
 355 360 365

Asp Val Leu Pro Gly Tyr Arg Asp Val Asp Ala Ala Gly Val Asp Leu
 370 375 380

Asp Ala Trp Phe Ala Asp Arg Asp Val Gln Ala Tyr Val Asp Arg Ile
 385 390 395 400

Asp Arg Gln Ser Ala Arg Leu Gly Ser Ala Ala Thr Val Thr Gly Ala
 405 410 415

Gly Leu Ser Ser Ala Pro Ser Ala Asp Ala Ser Ser Pro His Glu Ala
 420 425 430

Ala Leu Asp Asp Asp His Leu Pro Ala Glu Glu Ala Pro Ser Ser Asp
 435 440 445

Pro Ala Asn Gln Arg Leu Ser Asn Arg Leu Arg Trp Leu Ala Ala Ser
 450 455 460

Leu Val Val Gly Leu Val Ala Ala Leu Ala Ala Ala Val Met Leu Arg
 465 470 475 480

Pro Arg Glu Thr Ala Pro Val Val Leu Gln Pro Glu Pro Asp Arg Gln
 485 490 495

Asp Ala Val Glu Pro Lys Pro Ser Ala Gln Asp Ser Ala Thr Leu Lys
 500 505 510

Pro Gln Ala
 515

<210> 122
 <211> 525
 <212> PRT
 <213> Oryza sativa

<400> 122

Ala-Ala Glu Arg Ser Leu-Pro Leu Gln Val Asp Phe Tyr Lys Val Leu--
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Gly Ala Glu Pro His Phe Leu Gly Asp Gly Ile Arg Arg Ala Phe Glu
 20 25 30

Ala Arg Ile Ala Lys Pro Pro Gln Tyr Gly Tyr Ser Thr Asp Ala Leu
 35 40 45

Val Gly Arg Arg Gln Met Leu Gln Ile Ala His Asp Thr Leu Met Asn
 50 55 60

Gln Asn Ser Arg Thr Gln Tyr Asp Arg Ala Leu Ser Glu Asn Arg Glu
 65 70 75 80

Glu Ala Leu Thr Met Asp Ile Ala Trp Asp Lys Glu Ala Gly Glu Ala
 85 90 95

Leu Ala Val Leu Val Thr Gly Glu Gln Leu Leu Leu Asp Arg Pro Pro
 100 105 110

Lys Arg Phe Lys Gln Asp Val Val Leu Ala Met Ala Leu Ala Tyr Val
 115 120 125

Asp Leu Ser Arg Asp Ala Met Ala Ala Ser Pro Pro Asp Val Ile Gly
 130 135 140

Cys Cys Glu Val Leu Glu Arg Ala Leu Lys Leu Leu Gln Glu Asp Gly
 145 150 155 160

Ala Ser Asn Leu Ala Pro Asp Leu Leu Ser Gln Ile Asp Glu Thr Leu
 165 170 175

Glu Glu Ile Thr Pro Arg Cys Val Leu Glu Leu Leu Ser Leu Pro Ile
 180 185 190

Asp Thr Glu His His Lys Lys Arg Gln Glu Gly Leu Gln Gly Ala Arg
 195 200 205

Asn Ile Leu Trp Ser Val Gly Arg Gly Gly Ile Ala Thr Val Gly Gly
 210 215 220

Gly Phe Ser Arg Glu Ala Phe Met Asn Glu Ala Phe Leu Arg Met Thr
 225 230 235 240

Ser Ile Glu Gln Met Asp Phe Phe Ser Lys Thr Pro Asn Ser Ile Pro
 245 250 255

Pro Glu Trp Phe Glu Ile Tyr Asn Val Ala Leu Ala His Val Ala Gln
 260 265 270

Ala Ile Ile Ser Lys Arg Pro Gln Phe Ile Met Met Ala Asp Asp Leu
 275 280 285

Phe Glu Gln Leu Gln Lys Phe Asn Ile Gly Ser His Tyr Ala Tyr Asp
 290 295 300

Asn Glu Met Asp Leu Ala Leu Glu Arg Ala Phe Cys Ser Leu Leu Val
 305 310 315 320

Gly Asp Val Ser Lys Cys Arg Met Trp Leu Gly Ile Asp Asn Glu Ser
 325 330 335

Ser Pro Tyr Arg Asp Pro Lys Ile Leu Glu Phe Ile Val Thr Asn Ser
 340 345 350

Ser Ile Ser Glu Glu Asn Asp Leu Leu Pro Gly Leu Cys Lys Leu Leu
 355 360 365

Glu Thr Trp Leu Ile Phe Glu Val Phe Pro Arg Ser Arg Asp Thr Arg
 370 375 380

Gly Met Gln Phe Arg Leu Gly Asp Tyr Tyr Asp Asp Pro Glu Val Leu
 385 390 395 400

Ser Tyr Leu Glu Arg Met Glu Gly Gly Gly Ala Ser His Leu Ala Ala
 405 410 415

Ala Ala Ala Ile Ala Lys Leu Gly Ala Gln Ala Thr Ala Ala Leu Gly

420	425	430
Thr Val Lys Ser Asn Ala Ile Gln Ala Phe Asn Lys Val Phe Pro Leu		
435	440	445
Ile Glu Gln Leu Asp Arg Ser Ala Met Glu Asn Thr Lys Asp Gly Pro		
450	455	460
Gly Gly Tyr Leu Glu Asn Phe Asp Gln Glu Asn Ala Pro Ala His Asp		
465	470	475
Ser Arg Asn Ala Ala Leu Lys Ile Ile Ser Ala Gly Ala Leu Phe Ala		
	485	490
Leu Leu Ala Val Ile Gly Ala Lys Tyr Leu Pro Arg Lys Arg Pro Leu		
	500	510
Ser Ala Ile Arg Ser Glu His Gly Ser Val Ala Val Ala		
	515	520
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Gly Ala Gln Thr His Phe Leu Thr Asp Gly Ile Arg Arg Ala Phe Glu		
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Ala Arg Val Ser Lys Pro Pro Gln Phe Gly Phe Ser Asp Asp Ala Leu		
	35	40
Ile Ser Arg Arg Gln Ile Leu Gln Ala Ala Cys Glu Thr Leu Ser Asn		
	50	55
Pro Arg Ser Arg Arg Glu Tyr Asn Glu Gly Leu Leu Asp Asp Glu Glu		
65	70	75
Ala Thr Val Ile Thr Asp Val Pro Trp Asp Lys Val Pro Gly Ala Leu		
	85	90
Cys Val Leu Gln Glu Gly Gly Glu Thr Glu Ile Val Leu Arg Val Gly		
	100	110

Glu Ala Leu Leu Lys Glu Arg Leu Pro Lys Ser Phe Lys Gln Asp Val
 115 120 125

Val Leu Val Met Ala Leu Ala Phe Leu Asp Val Ser Arg Asp Ala Met
 130 135 140

Ala Leu Asp Pro Pro Asp Phe Ile Thr Gly Tyr Glu Phe Val Glu Glu
 145 150 155 160

Ala Leu Lys Leu Leu Gln Glu Glu Gly Ala Ser Ser Leu Ala Pro Asp
 165 170 175

Leu Arg Ala Gln Ile Asp Glu Thr Leu Glu Glu Ile Thr Pro Arg Tyr
 180 185 190

Val Leu Glu Leu Leu Gly Leu Pro Leu Gly Asp Asp Tyr Ala Ala Lys
 195 200 205

Arg Leu Asn Gly Leu Ser Gly Val Arg Asn Ile Leu Trp Ser Val Gly
 210 215 220

Gly Gly Gly Ala Ser Ala Leu Val Gly Gly Leu Thr Arg Glu Lys Phe
 225 230 235 240

Met Asn Glu Ala Phe Leu Arg Met Thr Ala Ala Glu Gln Val Asp Leu
 245 250 255

Phe Val Ala Thr Pro Ser Asn Ile Pro Ala Glu Ser Phe Glu Val Tyr
 260 265 270

Glu Val Ala Leu Ala Leu Val Ala Gln Ala Phe Ile Gly Lys Lys Pro
 275 280 285

His Leu Leu Gln Asp Ala Asp Lys Gln Phe Gln Gln Leu Gln Gln Ala
 290 295 300

Lys Val Met Ala Met Glu Ile Pro Ala Met Leu Tyr Asp Thr Arg Asn
 305 310 315 320

Asn Trp Glu Ile Asp Phe Gly Leu Glu Arg Gly Leu Cys Ala Leu Leu
 325 330 335

Ile Gly Lys Val Asp Glu Cys Arg Met Trp Leu Gly Leu Asp Ser Glu
 340 345 350

Asp Ser Gln Tyr Arg Asn Pro Ala Ile Val Glu Phe Val Leu Glu Asn
 355 360 365

Ser Asn Arg Asp Asp Asn Asp Asp Leu Pro Gly Leu Cys Lys Leu Leu
 370 375 380

Glu Thr Trp Leu Ala Gly Val Val Phe Pro Arg Phe Arg Asp Thr Lys
 385 390 395 400

Asp Lys Lys Phe Lys Leu Gly Asp Tyr Tyr Asp Asp Pro Met Val Leu
 405 410 415

Ser Tyr Leu Glu Arg Val Glu Val Val Gln Gly Ser Pro Leu Ala Ala
 420 425 430

Ala Ala Ala Met Ala Arg Ile Gly Ala Glu His Val Lys Ala Ser Ala
 435 440 445

Met Gln Ala Leu Gln Lys Val Phe Pro Ser Arg Tyr Thr Asp Arg Asn
 450 455 460

Ser Ala Glu Pro Lys Asp Val Gln Glu Thr Val Phe Ser Val Asp Pro
 465 470 475 480

Val Gly Asn Asn Val Gly Arg Asp Gly Glu Pro Gly Val Phe Ile Ala
 485 490 495

Glu Ala Val Arg Pro Ser Glu Asn Phe Glu Thr Asn Asp Tyr Ala Ile
 500 505 510

Arg Ala Gly Val Ser Glu Ser Ser Val Asp Glu Thr Thr Val Glu Met
 515 520 525

Ser Val Ala Asp Met Leu Lys Glu Ala Ser Val Lys Ile Leu Ala Ala
 530 535 540

Gly Val Ala Ile Gly Leu Ile Ser Leu Phe Ser Gln Lys Tyr Phe Leu
 545 550 555 560

Lys Ser Ser Ser Ser Phe Gln Arg Lys Asp Met Val Ser Ser Met Glu
 565 570 575

Ser Asp

<210> 124
 <211> 99
 <212> PRT
 <213> Solanum tuberosum

<400> 124

Pro Ser Asp His His Ile Ser Met Pro Ile Asp Phe Tyr Arg Val Leu
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Gly Ala Glu Ala His Phe Leu Gly Asp Gly Ile Arg Arg Cys Tyr Asp
20 25 30

Ala Arg Ile Thr Lys Pro Pro Gln Tyr Gly Tyr Ser Gln Glu Ala Leu
35 40 45

Ile Gly Arg Arg Gln Ile Leu Gln Ala Ala Cys Glu Thr Leu Ala Asp
50 55 60

Ser Thr Ser Arg Arg Glu Tyr Asn Gln Gly Leu Ala Gln His Glu Phe
65 70 75 80

Asp Thr Ile Leu Thr Pro Val Pro Trp Asp Lys Val Pro Gly Ala Met
85 90 95

Cys Val Leu

<210> 125

<211> 760

<212> PRT

<213> Oryza sativa

<400> 125

Met Glu Gly Phe His Asn Leu Leu Ala Arg Pro Asn Ser Ala Pro Phe
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Ala Phe Ser Leu Pro Arg Pro Arg Pro Arg Pro Arg Arg Arg Pro Pro
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Pro His Pro Ser Ala Ala Cys Arg Ala Ala Ser Arg Trp Ala Glu Arg
35 40 45

Leu Phe Ala Asp Phe His Leu Leu Pro Thr Ala Ala Pro Ser Asp Pro
50 55 60

Pro Ser Pro Ala Pro Ala Pro Ala Ala Pro Ser Ala Ser Pro Phe
65 70 75 80

Val Pro Leu Phe Pro Asp Ala Ala Glu Arg Ser Leu Pro Leu Gln Val
85 90 95

Asp Phe Tyr Lys Val Leu Gly Ala Glu Pro His Phe Leu Gly Asp Gly

-109-

Leu Ala His Val Ala Gln Ala Ile Ile Ser Lys Arg Pro Gln Phe Ile
 355 360 365

Met Met Ala Asp Asp Leu Phe Glu Gln Leu Gln Lys Phe Asn Ile Gly
 370 375 380

Ser His Tyr Ala Tyr Asp Asn Glu Met Asp Leu Ala Leu Glu Arg Ala
 385 390 395 400

Phe Cys Ser Leu Leu Val Gly Asp Val Ser Lys Cys Arg Met Trp Leu
 405 410 415

Gly Ile Asp Asn Glu Ser Ser Pro Tyr Arg Asp Pro Lys Ile Leu Glu
 420 425 430

Phe Ile Val Thr Asn Ser Ser Ile Ser Glu Glu Asn Asp Leu Leu Pro
 435 440 445

Gly Leu Cys Lys Leu Leu Glu Thr Trp Leu Ile Phe Glu Val Phe Pro
 450 455 460

Arg Ser Arg Asp Thr Arg Gly Met Gln Phe Arg Leu Gly Asp Tyr Tyr
 465 470 475 480

Asp Asp Pro Glu Val Leu Ser Tyr Leu Glu Arg Met Glu Gly Gly Gly
 485 490 495

Ala Ser His Leu Ala Ala Ala Ala Ala Ile Ala Lys Leu Gly Ala Gln
 500 505 510

Ala Thr Ala Ala Leu Gly Thr Val Lys Ser Asn Ala Ile Gln Ala Phe
 515 520 525

Asn Lys Val Phe Pro Leu Ile Glu Gln Leu Asp Arg Ser Ala Met Glu
 530 535 540

Asn Thr Lys Asp Gly Pro Gly Gly Tyr Leu Glu Asn Phe Asp Gln Glu
 545 550 555 560

Asn Ala Pro Ala His Asp Ser Arg Asn Ala Ala Leu Lys Ile Ile Ser
 565 570 575

Ala Gly Ala Leu Phe Ala Leu Leu Ala Val Ile Gly Ala Lys Tyr Leu
 580 585 590

Pro Arg Lys Arg Pro Leu Ser Ala Ile Arg Ser Glu His Gly Ser Val
 595 600 605

Ala Val Ala Asn Ser Val Asp Ser Thr Asp Asp Pro Ala Leu Asp Glu
610 615 620

Asp Pro Val His Ile Pro Arg Met Asp Ala Lys Leu Ala Glu Asp Ile
625 630 635 640

Val Arg Lys Trp Gln Ser Ile Lys Ser Lys Ala Leu Gly Pro Glu His
645 650 655

Ser Val Ala Ser Leu Gln Glu Val Leu Asp Gly Asn Met Leu Lys Val
660 665 670

Trp Thr Asp Arg Ala Ala Glu Ile Glu Arg His Gly Trp Phe Trp Glu
675 680 685

Tyr Thr Leu Ser Asp Val Thr Ile Asp Ser Ile Thr Ile Ser Leu Asp
690 695 700

Gly Arg Arg Ala Thr Val Glu Ala Thr Ile Asp Glu Ala Gly Gln Leu
705 710 715 720

Thr Asp Val Thr Glu Pro Arg Asn Asn Asp Ser Tyr Asp Thr Lys Tyr
725 730 735

Thr Thr Arg Tyr Glu Met Ala Phe Ser Lys Leu Gly Gly Trp Lys Ile
740 745 750

Thr Glu Gly Ala Val Leu Lys Ser
755 760

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<213> Oryza sativa

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<400> 127

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Asp Phe Asn Phe Thr Ser Asp Ser Ser Ser Ser Ser Phe Ala Thr Ala
 50 55 60

Thr Thr Thr Ala Thr Leu Val Ser Pro Pro Pro Ser Ile Asp Arg Pro
 65 70 75 80

Glu Arg His Val Pro Ile Pro Ile Asp Phe Tyr Gln Val Leu Gly Ala
 85 90 95

Gln Thr His Phe Leu Thr Asp Gly Ile Arg Arg Ala Phe Glu Ala Arg
 100 105 110

Val Ser Lys Pro Pro Gln Phe Gly Phe Ser Asp Asp Ala Leu Ile Ser
 115 120 125

Arg Arg Gln Ile Leu Gln Ala Ala Cys Glu Thr Leu Ser Asn Pro Arg
 130 135 140

Ser Arg Arg Glu Tyr Asn Glu Gly Leu Leu Asp Asp Glu Glu Ala Thr
 145 150 155 160

Val Ile Thr Asp Val Pro Trp Asp Lys Val Pro Gly Ala Leu Cys Val
 165 170 175

Leu Gln Glu Gly Gly Glu Thr Glu Ile Val Leu Arg Val Gly Glu Ala
 180 185 190

Leu Leu Lys Glu Arg Leu Pro Lys Ser Phe Lys Gln Asp Val Val Leu
 195 200 205

Val Met Ala Leu Ala Phe Leu Asp Val Ser Arg Asp Ala Met Ala Leu
 210 215 220

Asp Pro Pro Asp Phe Ile Thr Gly Tyr Glu Phe Val Glu Glu Ala Leu
 225 230 235 240
 Lys Leu Leu Gln Glu Glu Gly Ala Ser Ser Leu Ala Pro Asp Leu Arg
 245 250 255
 Ala Gln Ile Asp Glu Thr Leu Glu Glu Ile Thr Pro Arg Tyr Val Leu
 260 265 270
 Glu Leu Leu Gly Leu Pro Leu Gly Asp Asp Tyr Ala Ala Lys Arg Leu
 275 280 285
 Asn Gly Leu Ser Gly Val Arg Asn Ile Leu Trp Ser Val Gly Gly Gly
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 Gly Ala Ser Ala Leu Val Gly Gly Leu Thr Arg Glu-Lys Phe Met Asn
 305 310 315 320
 Glu Ala Phe Leu Arg Met Thr Ala Ala Glu Gln Val Asp Leu Phe Val
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 Ala Thr Pro Ser Asn Ile Pro Ala Glu Ser Phe Glu Val Tyr Glu Val
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 Ala Leu Ala Leu Val Ala Gln Ala Phe Ile Gly Lys Lys Pro His Leu
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 Leu Gln Asp Ala Asp Lys Gln Phe Gln Gln Leu Gln Gln Ala Lys Val
 370 375 380
 Met Ala Met Glu Ile Pro Ala Met Leu Tyr Asp Thr Arg Asn Asn Trp
 385 390 395 400
 Glu Ile Asp Phe Gly Leu Glu Arg Gly Leu Cys Ala Leu Leu Ile Gly
 405 410 415
 Lys Val Asp Glu Cys Arg Met Trp Leu Gly Leu Asp Ser Glu Asp Ser
 420 425 430
 Gln Tyr Arg Asn Pro Ala Ile Val Glu Phe Val Leu Glu Asn Ser Asn
 435 440 445
 Arg Asp Asp Asn Asp Asp Leu Pro Gly Leu Cys Lys Leu Leu Glu Thr
 450 455 460
 Trp Leu Ala Gly Val Val Phe Pro Arg Phe Arg Asp Thr Lys Asp Lys
 465 470 475 480

Lys Phe Lys Leu Gly Asp Tyr Tyr Asp Asp Pro Met Val Leu Ser Tyr
485 490 495

Leu Glu Arg Val Glu Val Val Gln Gly Ser Pro Leu Ala Ala Ala Ala
500 505 510

Ala Met Ala Arg Ile Gly Ala Glu His Val Lys Ala Ser Ala Met Gln
515 520 525

Ala Leu Gln Lys Val Phe Pro Ser Arg Tyr Thr Asp Arg Asn Ser Ala
530 535 540

Glu Pro Lys Asp Val Gln Glu Thr Val Phe Ser Val Asp Pro Val Gly
545 550 555 560

Asn Asn Val Gly Arg Asp Gly Glu Pro Gly Val Phe Ile Ala Glu Ala
565 570 575

Val Arg Pro Ser Glu Asn Phe Glu Thr Asn Asp Tyr Ala Ile Arg Ala
580 585 590

Gly Val Ser Glu Ser Ser Val Asp Glu Thr Thr Val Glu Met Ser Val
595 600 605

Ala Asp Met Leu Lys Glu Ala Ser Val Lys Ile Leu Ala Ala Gly Val
610 615 620

Ala Ile Gly Leu Ile Ser Leu Phe Ser Gln Lys Tyr Phe Leu Lys Ser
625 630 635 640

Ser Ser Ser Phe Gln Arg Lys Asp Met Val Ser Ser Met Glu Ser Asp
645 650 655

Val Ala Thr Ile Gly Ser Val Arg Ala Asp Asp Ser Glu Ala Leu Pro
660 665 670

Arg Met Asp Ala Arg Thr Ala Glu Asn Ile Val Ser Lys Trp Gln Lys
675 680 685

Ile Lys Ser Leu Ala Phe Gly Pro Asp His Arg Ile Glu Met Leu Pro
690 695 700

Glu Val Leu Asp Gly Arg Met Leu Lys Ile Trp Thr Asp Arg Ala Ala
705 710 715 720

Glu Thr Ala Gln Leu Gly Leu Val Tyr Asp Tyr Thr Leu Leu Lys Leu

725

730

735

Ser Val Asp Ser Val Thr Val Ser Ala Asp Gly Thr Arg Ala Leu Val
740 745 750

Glu Ala Thr Leu Glu Glu Ser Ala Cys Leu Ser Asp Leu Val His Pro
755 760 765

Glu Asn Asn Ala Thr Asp Val Arg Thr Tyr Thr Thr Arg Tyr Glu Val
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Phe Trp Ser Lys Ser Gly Trp Lys Ile Thr Glu Gly Ser Val Leu Ala
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Ser

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<211> 2406

<212> DNA

<213> Arabidopsis thaliana

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aatatagtat	ccaagtggca	gaagattaag	tctctggctt	ttgggcctga	tcaccgcata	2100
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gaaactgcgc	agcttgggtt	ggtttatgat	tataactgt	tgaaactatc	tgttgacagt	2220
gtgacagtct	cagcagatgg	aaccctgtct	ctgggtggaag	caactctgga	ggagtctgct	2280
tgtctatctg	atttggttca	tccagaaaac	aatgctactg	atgtcagaac	ctacacaaca	2340
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<210> 129
 <211> 801
 <212> PRT
 <213> Arabidopsis thaliana

<400> 129

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Cys	Arg	Leu	Pro	Pro	Ala	Thr	Thr	Lys	Leu	Arg	Arg	Ser	His	Asn	Thr
			20					25					30		

Ser Thr Thr Ile Cys Ser Ala Ser Lys Trp Ala Asp Arg Leu Leu Ser
35 40 45

Asp Phe Asn Phe Thr Ser Asp Ser Ser Ser Ser Ser Phe Ala Thr Ala
50 55 60

Thr Thr Thr Ala Thr Leu Val Ser Pro Pro Pro Ser Ile Asp Arg Pro
65 70 75 80

Glu Arg His Val Pro Ile Pro Ile Asp Phe Tyr Gln Val Leu Gly Ala
85 90 95

Gln Thr His Phe Leu Thr Asp Gly Ile Arg Arg Ala Phe Glu Ala Arg
100 105 110

Val Ser Lys Pro Pro Gln Phe Gly Phe Ser Asp Asp Ala Leu Ile Ser
115 120 125

Arg Arg Gln Ile Leu Gln Ala Ala Cys Glu Thr Leu Ser Asn Pro Arg
130 135 140

Ser Arg Arg Glu Tyr Asn Glu Gly Leu Leu Asp Asp Glu Glu Ala Thr
145 150 155 160

Val Ile Thr Asp Val Pro Trp Asp Lys Val Pro Gly Ala Leu Cys Val
165 170 175

Leu Gln Glu Gly Gly Glu Thr Glu Ile Val Leu Arg Val Gly Glu Ala
180 185 190

Leu Leu Lys Glu Arg Leu Pro Lys Ser Phe Lys Gln Asp Val Val Leu
195 200 205

Val Met Ala Leu Ala Phe Leu Asp Val Ser Arg Asp Ala Met Ala Leu
210 215 220

Asp Pro Pro Asp Phe Ile Thr Gly Tyr Glu Phe Val Glu Glu Ala Leu
225 230 235 240

Lys Leu Leu Gln Glu Glu Gly Ala Ser Ser Leu Ala Pro Asp Leu Arg
245 250 255

Ala Gln Ile Asp Glu Thr Leu Glu Glu Ile Thr Pro Arg Tyr Val Leu
260 265 270

Glu Leu Leu Gly Leu Pro Leu Gly Asp Asp Tyr Ala Ala Lys Arg Leu

275					280					285					
Asn	Gly	Leu	Ser	Gly	Val	Arg	Asn	Ile	Leu	Trp	Ser	Val	Gly	Gly	Gly
290						295					300				
Gly	Ala	Ser	Ala	Leu	Val	Gly	Gly	Leu	Thr	Arg	Glu	Lys	Phe	Met	Asn
305					310					315					320
Glu	Ala	Phe	Leu	Arg	Met	Thr	Ala	Ala	Glu	Gln	Val	Asp	Leu	Phe	Val
				325					330					335	
Ala	Thr	Pro	Ser	Asn	Ile	Pro	Ala	Glu	Ser	Phe	Glu	Val	Tyr	Glu	Val
			340					345					350		
Ala	Leu	Ala	Leu	Val	Ala	Gln	Ala	Phe	Ile	Gly	Lys	Lys	Pro	His	Leu
		355					360					365			
Leu	Gln	Asp	Ala	Asp	Lys	Gln	Phe	Gln	Gln	Leu	Gln	Gln	Ala	Lys	Val
	370					375					380				
Met	Ala	Met	Glu	Ile	Pro	Ala	Met	Leu	Tyr	Asp	Thr	Arg	Asn	Asn	Trp
385					390					395					400
Glu	Ile	Asp	Phe	Gly	Leu	Glu	Arg	Gly	Leu	Cys	Ala	Leu	Leu	Ile	Gly
				405					410					415	
Lys	Val	Asp	Glu	Cys	Arg	Met	Trp	Leu	Gly	Leu	Asp	Ser	Glu	Asp	Ser
			420					425					430		
Gln	Tyr	Arg	Asn	Pro	Ala	Ile	Val	Glu	Phe	Val	Leu	Glu	Asn	Ser	Asn
		435					440					445			
Arg	Asp	Asp	Asn	Asp	Asp	Leu	Pro	Gly	Leu	Cys	Lys	Leu	Leu	Glu	Thr
	450					455					460				
Trp	Leu	Ala	Gly	Val	Val	Phe	Pro	Arg	Phe	Arg	Asp	Thr	Lys	Asp	Lys
465					470					475					480
Lys	Phe	Lys	Leu	Gly	Asp	Tyr	Tyr	Asp	Asp	Pro	Met	Val	Leu	Ser	Tyr
				485					490					495	
Leu	Glu	Arg	Val	Glu	Val	Val	Gln	Gly	Ser	Pro	Leu	Ala	Ala	Ala	Ala
			500					505					510		
Ala	Met	Ala	Arg	Ile	Gly	Ala	Glu	His	Val	Lys	Ala	Ser	Ala	Met	Gln
		515					520					525			

Ala Leu Gln Lys Val Phe Pro Ser Arg Tyr Thr Asp Arg Asn Ser Ala
530 535 540

Glu Pro Lys Asp Val Gln Glu Thr Val Phe Ser Val Asp Pro Val Gly
545 550 555 560

Asn Asn Val Gly Arg Asp Gly Glu Pro Gly Val Phe Ile Ala Glu Ala
565 570 575

Val Arg Pro Ser Glu Asn Phe Glu Thr Asn Asp Tyr Ala Ile Arg Ala
580 585 590

Gly Val Ser Glu Ser Ser Val Asp Glu Thr Thr Val Glu Met Ser Val
595 600 605

Ala Asp Met Leu Lys Glu Ala Ser Val Lys Ile Leu Ala Ala Gly Val
610 615 620

Ala Ile Gly Leu Ile Ser Leu Phe Ser Gln Lys Tyr Phe Leu Lys Ser
625 630 635 640

Ser Ser Ser Phe Gln Arg Lys Asp Met Val Ser Ser Met Glu Ser Asp
645 650 655

Val Ala Thr Ile Gly Ser Val Arg Ala Asp Asp Ser Glu Ala Leu Pro
660 665 670

Arg Met Asp Ala Arg Thr Ala Glu Asn Ile Val Ser Lys Trp Gln Lys
675 680 685

Ile Lys Ser Leu Ala Phe Gly Pro Asp His Arg Ile Glu Met Leu Pro
690 695 700

Glu Val Leu Asp Gly Arg Met Leu Lys Ile Trp Thr Asp Arg Ala Ala
705 710 715 720

Glu Thr Ala Gln Leu Gly Leu Val Tyr Asp Tyr Thr Leu Leu Lys Leu
725 730 735

Ser Val Asp Ser Val Thr Val Ser Ala Asp Gly Thr Arg Ala Leu Val
740 745 750

Glu Ala Thr Leu Glu Glu Ser Ala Cys Leu Ser Asp Leu Val His Pro
755 760 765

Glu Asn Asn Ala Thr Asp Val Arg Thr Tyr Thr Thr Arg Tyr Glu Val
770 775 780

Phe	Trp	Ser	Lys	Ser	Gly	Trp	Lys	Ile	Thr	Glu	Gly	Ser	Val	Leu	Ala
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Ser

<210> 130
 <211> 2637
 <212> DNA
 <213> Arabidopsis thaliana

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<400> 130
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ctctgagtca cgtcggcatt ggtctctccc cattccaatt atgccgatta ccaccggcga      180
cgacaaaagct ccgacgtagc cacaacacct ctacaactat ctgctccgcc agcaaatggg      240
ccgaccgtct tctctccgac ttcaatttca cctccgattc ctctctctcc tccttcgccca      300
ccgccaccac caccgccact ctgctctctc cgccaccatc tattgatcgt cccgaacgcc      360
acgtcccatc cccattgat ttctaccagg tattaggagc tcaaacacat ttcttaaccg      420
atggaatcag aagagcattc gaagctaggg ttctgaaaacc gccgcaattc ggtttcagcg      480
acgacgcttt aatcagccgg agacagattc ttcaagctgc ttgcgaaact ctgtctaact      540
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ctgatgttcc ttgggataag gttcctgggtg ctctctgtgt attgcaagaa ggtggtgaga      660
ctgagatagt tcttcggggtt ggtgaggctc tgcttaagga gaggttgctt aagtcgttta      720
agcaagatgt ggttttagtt atggcgcttg cgtttctcga tgtctcgagg gatgctatgg      780
cattggatcc acctgatttt ataactgggtt atgagtttgt tgaggaagct ttgaagcttt      840
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tggaagagat cactccgcgt tatgtcttgg agctacttgg cttaccgctt ggtgatgatt      960
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gaggtggagc atcagctctt gttggggggt tgaccctgta gaagtttatg aatgaggcgt     1080
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cagcagagtc atttgaagtt tacgaagttg cacttgctct tgtggctcaa gcttttattg     1200
gtaagaagcc acacctttta caggatgctg ataagcaatt ccagcaactt cagcaggcta     1260
aggtaatggc tatggagatt cctgcgatgt tgtatgatac acggaataat tgggagatag     1320
acttcggtct agaaagggga ctctgtgcac tgcttatagg caaagttgat gaatgccgta     1380
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<210> 131
<211> 801
<212> PRT
<213> Arabidopsis thaliana

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<400> 131

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Cys Arg Leu Pro Pro Ala Thr Thr Lys Leu Arg Arg Ser His Asn Thr
20           25           30

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Ser Thr Thr Ile Cys Ser Ala Ser Lys Trp Ala Asp Arg Leu Leu Ser
35           40           45

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Asp Phe Asn Phe Thr Ser Asp Ser Ser Ser Ser Ser Phe Ala Thr Ala
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Thr Thr Thr Ala Thr Leu Val Ser Pro Pro Pro Ser Ile Asp Arg Pro
65 70 75 80

Glu Arg His Val Pro Ile Pro Ile Asp Phe Tyr Gln Val Leu Gly Ala
85 90 95

Gln Thr His Phe Leu Thr Asp Gly Ile Arg Arg Ala Phe Glu Ala Arg
100 105 110

Val Ser Lys Pro Pro Gln Phe Gly Phe Ser Asp Asp Ala Leu Ile Ser
115 120 125

Arg Arg Gln Ile Leu Gln Ala Ala Cys Glu Thr Leu Ser Asn Pro Arg
130 135 140

Ser Arg Arg Glu Tyr Asn Glu Gly Leu Leu Asp Asp Glu Glu Ala Thr
145 150 155 160

Val Ile Thr Asp Val Pro Trp Asp Lys Val Pro Gly Ala Leu Cys Val
165 170 175

Leu Gln Glu Gly Gly Glu Thr Glu Ile Val Leu Arg Val Gly Glu Ala
180 185 190

Leu Leu Lys Glu Arg Leu Pro Lys Ser Phe Lys Gln Asp Val Val Leu
195 200 205

Val Met Ala Leu Ala Phe Leu Asp Val Ser Arg Asp Ala Met Ala Leu
210 215 220

Asp Pro Pro Asp Phe Ile Thr Gly Tyr Glu Phe Val Glu Glu Ala Leu
225 230 235 240

Lys Leu Leu Gln Glu Glu Gly Ala Ser Ser Leu Ala Pro Asp Leu Arg
245 250 255

Ala Gln Ile Asp Glu Thr Leu Glu Glu Ile Thr Pro Arg Tyr Val Leu
260 265 270

Glu Leu Leu Gly Leu Pro Leu Gly Asp Asp Tyr Ala Ala Lys Arg Leu
275 280 285

Asn Gly Leu Ser Gly Val Arg Asn Ile Leu Trp Ser Val Gly Gly Gly
290 295 300

Gly Ala Ser Ala Leu Val Gly Gly Leu Thr Arg Glu Lys Phe Met Asn

305		310		315		320
Glu Ala Phe Leu Arg Met Thr Ala Ala Glu Gln Val Asp Leu Phe Val						
		325		330		335
Ala Thr Pro Ser Asn Ile Pro Ala Glu Ser Phe Glu Val Tyr Glu Val						
		340		345		350
Ala Leu Ala Leu Val Ala Gln Ala Phe Ile Gly Lys Lys Pro His Leu						
		355		360		365
Leu Gln Asp Ala Asp Lys Gln Phe Gln Gln Leu Gln Gln Ala Lys Val						
		370		375		380
Met Ala Met Glu Ile Pro Ala Met Leu Tyr Asp Thr Arg Asn Asn Trp						
385		390		395		400
Glu Ile Asp Phe Gly Leu Glu Arg Gly Leu Cys Ala Leu Leu Ile Gly						
		405		410		415
Lys Val Asp Glu Cys Arg Met Trp Leu Gly Leu Asp Ser Glu Asp Ser						
		420		425		430
Gln Tyr Arg Asn Pro Ala Ile Val Glu Phe Val Leu Glu Asn Ser Asn						
		435		440		445
Arg Asp Asp Asn Asp Asp Leu Pro Gly Leu Cys Lys Leu Leu Glu Thr						
		450		455		460
Trp Leu Ala Gly Val Val Phe Pro Arg Phe Arg Asp Thr Lys Asp Lys						
		465		470		475
Lys Phe Lys Leu Gly Asp Tyr Tyr Asp Asp Pro Met Val Leu Ser Tyr						
		485		490		495
Leu Glu Arg Val Glu Val Val Gln Gly Ser Pro Leu Ala Ala Ala Ala						
		500		505		510
Ala Met Ala Arg Ile Gly Ala Glu His Val Lys Ala Ser Ala Met Gln						
		515		520		525
Ala Leu Gln Lys Val Phe Pro Ser Arg Tyr Thr Asp Arg Asn Ser Ala						
		530		535		540
Glu Pro Lys Asp Val Gln Glu Thr Val Phe Ser Val Asp Pro Val Gly						
		545		550		555
						560

Asn Asn Val Gly Arg Asp Gly Glu Pro Gly Val Phe Ile Ala Glu Ala
565 570 575

Val Arg Pro Ser Glu Asn Phe Glu Thr Asn Asp Tyr Ala Ile Arg Ala
580 585 590

Gly Val Ser Glu Ser Ser Val Asp Glu Thr Thr Val Glu Met Ser Val
595 600 605

Ala Asp Met Leu Lys Glu Ala Ser Val Lys Ile Leu Ala Ala Gly Val
610 615 620

Ala Ile Gly Leu Ile Ser Leu Phe Ser Gln Lys Tyr Phe Leu Lys Ser
625 630 635 640

--- Ser Ser Ser Phe Gln Arg Lys Asp Met Val Ser Ser Met Glu Ser Asp
645 650 655

Val Ala Thr Ile Gly Ser Val Arg Ala Asp Asp Ser Glu Ala Leu Pro
660 665 670

Arg Met Asp Ala Arg Thr Ala Glu Asn Ile Val Ser Lys Trp Gln Lys
675 680 685

Ile Lys Ser Leu Ala Phe Gly Pro Asp His Arg Ile Glu Met Leu Pro
690 695 700

Glu Val Leu Asp Gly Arg Met Leu Lys Ile Trp Thr Asp Arg Ala Ala
705 710 715 720

Glu Thr Ala Gln Leu Gly Leu Val Tyr Asp Tyr Thr Leu Leu Lys Leu
725 730 735

Ser Val Asp Ser Val Thr Val Ser Ala Asp Gly Thr Arg Ala Leu Val
740 745 750

Glu Ala Thr Leu Glu Glu Ser Ala Cys Leu Ser Asp Leu Val His Pro
755 760 765

Glu Asn Asn Ala Thr Asp Val Arg Thr Tyr Thr Thr Arg Tyr Glu Val
770 775 780

Phe Trp Ser Lys Ser Gly Trp Lys Ile Thr Glu Gly Ser Val Leu Ala
785 790 795 800

Ser

<210> 132
 <211> 561
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> misc feature
 <222> (127)..(127)
 <223> n is a, c, g, or t

<220>
 <221> misc feature
 <222> (520)..(520)
 <223> n is a, c, g, or t

<220>
 <221> misc feature
 <222> (541)..(541)
 <223> n is a, c, g, or t

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 tggaccngaa aacttcgtat cttgttgtgt aggttctgac atcagtagca ttgttttctg 180
 gatgaaccaa atcagataga caagcagact cctccagagt tgcttccacc agagcacggg 240
 ttccatctgc tgagactgtc aactgtcaa cagatagttt caacagtgtg taatcataaa 300
 ccaacccaag ctgcgcagtt tcagctgctc tgtcagtcca aatcttcagc attcgcccat 360
 ccaaaacctc tggtaacatt tctatgcggt gatcaggccc aaaagccaga gacttaatct 420
 tctgccactt ggatactata ttctctgcag tcctagcatc cattctggga agtgcttctg 480
 aatcgtcagc tctgactgac cctatggtag cgacatcagn ttccatagaa gaaaccatat 540
 ncttgcgttg aaaagatgag c 561

<210> 133
 <211> 295
 <212> DNA
 <213> Medicago truncatula

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 gtcctgtagg agatgaagaa ttaggagagc aactacaaaa aatgagtgca atgggtgcag 180
 aagctctagt ccgcaagtgg caatatatca catcccaagc ttttggacct gaccattgcc 240
 taggaagatt gcaagaggtg ttggacggcc aaatgttgaa gatatggact gatcg 295

<210> 134

<211> 527
 <212> DNA
 <213> Medicago truncatula

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 acaacttgga ggatctcaac atcgacagtg tgaccatata acagaatggg cggcgtgcag 180
 tagtggaaac aactctcaaa gagtctaccc acctcactgc tgttggtcat ccacagcatg 240
 ctacttccaa cagcagaacc tacacaacaa gatatgaaat gtctttttca gattcagggg 300
 ggaaaattat tgaaggagct gtccttgagt cgtaattagg ttttgtaata tgtaatatat 360
 gtcagggttag tacacttcaa tattaacccc ctcgagccta tgcccactgt cttgtatgta 420
 cctgttgttt tgtgcatttt tcaagcattt atgtagtcag gctgtaaata cttggagggg 480
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<210> 135
 <211> 660
 <212> DNA
 <213> Medicago truncatula

<400> 135
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 ccaccacctc cgccacagtc actctcactc cttcttaccc tcctccgata gaacgccacg 180
 tgtcactccc tctcgacctg tacaaaaatcc tcggcgccga aacgcatttt ctcggtgatg 240
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 aagctttgat tagtcgtcgt cagattcttc aagctgcttg tgaaacccta gctgatcctg 360
 cttctagaag agagtataat caaagcctcg tcgacgatga agacgaagat gaggaatctt 420
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<210> 136
 <211> 187
 <212> DNA
 <213> Glycine max

<400> 136
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cgcatTTgtt gacgtgtcaa gggatgcttg gcttgttcac cggatttcat tgcggctgtg 180
agatgct 187

<210> 137
<211> 608
<212> DNA
<213> Solanum tuberosum

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ccgttaacgg aggagctagt agtggtaccg gtggaacaag tagtttacct actaacttct 180
ccgctagtaa atgggcggat cgtcttctcg ccgatttcca attccttcct tccaccacca 240
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ctgcttgtga aacccttgct gactctacct ctcgtagaga gtacaatcaa ggcctcgctc 540
agcatgagtt cgatactatt ctaactcctg tcccctggga taaagttccg ggagcaatgt 600
gtgttttg 608

<210> 138
<211> 307
<212> DNA
<213> Populus balsamifera

<400> 138
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cttgttgccc aagctttcat tggtaaaaag cctcatctca tcacagatgc tgataaccta 180
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tccatggaaa accgtgatat tgactttggg ttggagaggg gctttgttca ctgcttgtag 300
gccagct 307

<210> 139
<211> 416
<212> DNA
<213> Mesembryanthemum crystallinum

<400> 139
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tccaatgctg ggtggaagat catagagggg gctgtcctcc aatcttaagc tgctggaaat	180
ccagtcttga atgtacatat tttcacatca tctgcacatt atgaatgaag gatggatatgt	240
gttttctgga cagtgggtatt tgatcatgtt gtgtttatgt ttgtaacaag ttttgatcat	300
tatcaaaaaag atcactcttg taagttagtt ttttccacaa taaatcaact atttatatga	360
aagtttttat atcaggacta cttgccttta cttatataaa ctttgagaaa tttttt	416

<210> 140
 <211> 465
 <212> DNA
 <213> Oryza sativa

<220>
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 <222> (113)..(113)
 <223> n is a, c, g, or t

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aaaatttttga ccaggaaaaat gcacctgctc atgattcgag aaatgccgcc ttgaagatta	240
tctctctggc gcactgtttg cactgttggc agtaattggg gccaaatatt tgccctegtaa	300
gaggccctt tctgctatta ggagtgaaca tggatctgtg gcagttgcta atagtgtcga	360
ctctactgat gatcctgcac tagatgaaga tccagtacat attcctagaa tggatgcgaa	420
gctggcagaa gatattgttc gcaagtggca gagtatcaaa tctaa	465

<210> 141
 <211> 309
 <212> DNA
 <213> Oryza sativa

<400> 141	
atcataagaa gcgccaagaa gggcttcaag gtgcgagaaa cattttgttg agcgttggca	60
gaggaggtat tgctaccgtt ggaggaggat tttctcgtga agccttcatg aacgaggctt	120
ttttgaggat gacatcaatt gaacagatgg atttcttttc aaaaacaccg aatagcatte	180
ctcctgaatg gtttgaaatt tacaatgtag cacttgcaca tgtcgtcaa gcaattataa	240
gtaaaaggcc acaattcatc atgatggcgg atgatctttt tgaacaacte cagaagttcc	300
acataggtc	309

<210> 142
 <211> 336
 <212> DNA

<213> Oryza sativa

<400> 142

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atcataagaa gcgccaagaa gggcttcaag gtgcgagaaa cattttgtgg agcgttggca      60
gaggaggtat tgctaccgtt ggaggaggat tttctcgtga agccttcatg aacgaggctt      120
ttttgaggat gacatcaatt gaacagatgg atttcttttc aaaaacaccg aatagcattc      180
ctcctgaatg gtttgaaatt tacaatgtag cacttgcaca tgctcgtcaa gcaattataa      240
gtaaaaggcc acaattcatc atgatggcgg atgatctttt tgaacaactc cagaagttca      300
acataggttc tcattatgct tatgataatg agatgg                                     336
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<210> 143

<211> 537

<212> DNA

<213> Triticum aestivum

<400> 143

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cagtgccttg aattggaggg cacttactgg aggaccgccc gccaagcgg ttcaagcagg      60
atgtggtgct ggcaatggcg ctgcgttatg tggatctatc aagggacgca atggcgggcta      120
gccctccaga tgtaatccgc tgctgtgagg tgcttgaaaag ggctctcaag cttttgcagg      180
aggatggggc aatcaatctc gcacctggtt tgctctcaca aattgatgaa actctggagg      240
atatcacacc tcgttgtgtt ttggagcttc ttgcccttcc tcttgatgaa aaacatcaga      300
atgaacacca agaaggtctt cgtggtgtga gaaacatttt gtggagtgtt ggagaggag      360
gtattggtac tgttggagga ggattttcgc gtgaagccta catgaatgaa gccttcctgc      420
agatgacatc ggcggagcag atggatttct tctcaaaaac accgaatagc ataccgcctg      480
aatggtttga aatctatagc gtggcacttg caaatgttgc tcaagcaatt gtaagta       537
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<210> 144

<211> 418

<212> DNA

<213> Triticum monococcum

<220>

<221> misc feature

<222> (144)..(144)

<223> n is a, c, g, or t

<220>

<221> misc feature

<222> (301)..(301)

<223> n is a, c, g, or t

<400> 144

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acacctcgtt gtgttttggg gcttcttgcc cttcctcttg atgaaaagca ccagagtaaa      60
cgccaagaag gtcttcgtgg tgtgagaaac attttgtgga gtgttggtag aggaggtatt      120
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gctactgttg gaggaggatt ttcncgtgaa gcctacatga atgaggcctt tttgcagatg	180
acatcagcgg agcagatgga tttcttttca aaaacgccaa atagcatacc acctgaatgg	240
tttgaaatct atagtgtggc actcgcaa at gttgctcaag caattgtaag taaaaggcca	300
nagctcatca tgggtggcaga tgatcttttc gaacagctcc agaagttcaa tataggttct	360
caatatgctt atgataatga attggatctt gtgttgga gggcactttg ctcattgc	418

<210> 145
 <211> 480
 <212> DNA
 <213> Hordeum vulgare

<400> 145	
gcgagcatga gtccgtggca gttgcta atg ttgttgactc aggtgatgat gacgaaccag	60
atgagcccat acagattcct aaaatggatg cgaagctggc agaagatatt gttcgcaagt	120
ggcagagcat caaatccaag gccttgggat cagatcattc tggtgcatca ttgcaagagg	180
ttcttgatgg caacatgctg aaggatgga cggaccgagc agcagagatc gagcgcaaag	240
gctggttctg ggactacacg ctgtccaacg tggcgatcga cagcatcacc gtctccctgg	300
acggacggcg ggcgaccgtg gaggcgacaa ttgaggaggc gggtcagctc accgacgcaa	360
ccgaccccag gaacgatgat ttgtacgaca ctaagtacac caccgggtac gagatggcct	420
tcaccggacc aggagggtgg aagataaccg aaggcgcagt cctcaagtcg tcatagggcg	480

<210> 146
 <211> 622
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> misc_feature
 <222> (11)..(12)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (14)..(14)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (65)..(65)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (88)..(88)
 <223> n is a, c, g, or t

<400> 146	
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cgagnaagca ccagagtaaa cgccaagnaa ggtcttcgtg gtgtgagaaa catcttctgg	120
agtgttggtta gaggaggtat tgctactgtt ggtggaggat tttcacggga agcctacatg	180
aatgaggcct ttttgcagat gacatcagct gagcagatgg atttcttttc aaaaacgccg	240
aatagcatac cacctgaatg gtttgaaatc tatagcgtgg cactcgcaaa tgttgctcaa	300
gcaattgtaa gtaaaaggcc agagctcatc atggtggcag atgatctttt cgaacagctc	360
cagaagttca atatcggttc tcaatatgct tatggtaacg agatggatct tgcgttgaa	420
agggcacttt gctcattgct tgtgggagac attagcaact gcagaacttg gcttgcgatt	480
gataatgaat cttcaccaca tagagacccg aaaattgtag agtttattgt gaacaactct	540
agcattgacc accaggagaa tgatcttctt ccaggcctgt gtaagctttt ggagacttgg	600
cttgtctcag aggttttccc ta	622

<210> 147
 <211> 604
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> misc_feature
 <222> (13)..(13)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (516)..(516)
 <223> n is a, c, g, or t

<400> 147	
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ctaaccaaac tatctccgtc ttccaaactg acaagagcct agactagact gcttatttac	180
acaccagaaa aacacgggag gaatcaatca acaagggtta ctgcacgctg aacgccctat	240
gacgacttga ggactgcgcc ttcggttatc ttccaccctc ctgggtccggg gaaggccatc	300
tcgtaccggg tgggtgtactt agtgtcgta aaatcatcgt tcctgggggtc ggttgcgctg	360
gtgagctgac ccgcctctc aattgtcgcc tccacggctc cccgccgtcc gtccaggag	420
acggtgatgc tgctgatgc cacgttgaa agcgtgtagt cccagaacca gcctttgcgc	480
tcaatctctg ctgctcggtc tgtccatacc ttcagnatgt tgccatcaag aacctcttgc	540
aatgatgcaa cagaatgatc tgatcccaag gccttggatt tgatgctctg ccacttgcca	600
acaa	604

<210> 148

<211> 653
 <212> DNA
 <213> Sorghum bicolor

<400> 148
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 gaaattccta gaatggatgc aaagttaggt gaagatattg ttcgcaagtg gcaaagtatc 120
 aagtccaagg ctttggggcc agaacacact gtcacggcat tgcaagagat cctcgatggc 180
 aacatgctga aggtatggat ggaccgagcc acagagattg agcgtcacgg ttggttctgg 240
 gaatacacac tctccgacgt gacgatcgac agtatcaccg tctccatgga cggtcgacgg 300
 gcaactgtgg aggcgacgat tgaggagatg ggccaactta ccgacgtagc agacccaaag 360
 aacaacgacg cctacgacac aaagtacacc gtcggttacg agatgagcta ctccaagtcc 420
 ggagggtgga ggatcaccga aggagcagtc ctcaagtcgt agaacggtcg tgcagcagga 480
 gtaggcgagt aggggttgct caactcccat tcttttttct tttgcaccag tgtatgtaaa 540
 taaacagtgt gagcacaggt tcttttctct cctggagaga gtttggttag gttgattagt 600
 gatgagttcc tgaggccgag agaatttgtc atctagtttg tattgataga gat 653

<210> 149
 <211> 535
 <212> DNA
 <213> Sorghum bicolor

<400> 149
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 aatctcttga aaaacttgcc caagaaatgt tgctggagat gctatccatg attccaaaaa 120
 tgccgctttg aagattatct ctgctggtgc actgtttgca ctatttgag taataggtct 180
 gaagtgcttg cctcgtaaga agtcacttcc tgctcttaag agcgaatatg ggtctgtggc 240
 agttgctgac tctgttgatg gtctgggagc agatgaagag ccactagaaa ttcctagaat 300
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 ggggccagaa cacactgtca cggcattgca agagatcctc gatggcaaca tgctgaaggt 420
 atggatggac cgagccacag agattgagcg tcacggttgg ttctgggaat acacactctc 480
 cgacgtgacg atcgacagta tcaccgtctc catggacggg cgacgggcaa ctgtg 535

<210> 150
 <211> 479
 <212> DNA
 <213> Zea mays

<400> 150
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cttctctctc	gtccccgttc	gtccccgatct	tccccgaagc	cgccgaccgc	gccttgcccc	180
tccccggtcga	cttctacaag	attcttggtg	cggagccaca	tttcctaggc	gatggcattc	240
ggagggcggtt	cgagtcgcgg	atagctaagc	cacctcagta	tgggtacagc	acagaagctc	300
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gcaccgagta	cgaccgtgcg	ctttccgagg	accgtgatgc	ggcactcacc	atggatgttg	420
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<210> 151
 <211> 446
 <212> DNA
 <213> Zea mays

<400> 151	
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gaaggcctca	cgagaaaaatc ctccctccaac agtagcaata ccacccctgc caacactcca 180
caatatgttt	tttgacacctt gcagaccttc ttggcgttta tttttatggt tttcatcagt 240
aggaagagca	agaagctcca atacacaacg aggtgtaatc tcctccaaag tttcatcaat 300
ctgtgcaagc	agttcagggtg caagattgct tgcaccatcc tcctgcagga gcttcagtgc 360
cctctcaagc	acctcacaac agcagattac atctggagggg cttgctgcca tagcatccct 420
tgatatgtcc	acataagcca atgcca 446

<210> 152
 <211> 657
 <212> DNA
 <213> Zea mays

<400> 152	
cgcgtcgacg	tatagagtct gcatccatgt tgcttgaat gaagcgtctg caaaagaagg 60
ctcttttatc	accagtcgtg tcaggaagca ttttgaaaat atatcaaaat ttctttggct 120
gagtgatagg	cctaattcaa atagcaaagg aagtgataaa caccagcgg ttaatgatat 180
tactgctgca	gtttgcaagc aaaagatgga tattcaagaa gcagaaacac ttgtaaaaca 240
gtggcaagac	ataaaaatctg aagctcttgg ccctgactat caaactgaca tgctacctga 300
gattcttgat	ggttcaatgc tctctaagtg ggaagactta gcgttattag caaaggacca 360
gtcttgetat	tggagatttg tgctgctaaa tcttaatggt gttcgagccg agataatctt 420
ggatgaaata	ggtgctgggtg aggcagcaga aattgatgct gtacttgagg aagcggctga 480
gcttgttgac	gattcccagc ccaagaaacc gagttattac agcacatatg aagttcagta 540
cgtattgagg	aggcagaatc atggatcttg gaaaatctcc gaggctgctg tccgggacct 600

gacgtgattt ctgccaaactc ggcaaacggg ctacacaacc attggcgtat aggcgge 657

<210> 153
 <211> 871
 <212> DNA
 <213> *Ceratopteris richardii*

<400> 153
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 ctcgaatgac agctgctgag caagtagctt tgttcacaaa tacaccagc aatatccag 120
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 ttatagctaa ttcttttgga agtgaggaag gtgattatgt accaggcctt tgcaagtgtg 480
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 aatgatggag tgtcattgtt gcttttgagg tgacgaagg gggcgctcc tctttaagg 720
 atcgtccgtg ggggcgcgcg ctcccatatc gccatcttcg ggacaccttg ttcgtgggtc 780
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 agcactctca gcttcgacga aacagcctaa a 871

<210> 154
 <211> 541
 <212> DNA
 <213> *Physcomitrella patens*

<400> 154
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 ggctcttcct gaggtgctgg agggcgagat gctgaagage tggacagacc gtgttagtga 180
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 ttgattctga gattttcatc tccggatcat gttgacttgt aggcagatcg actagttgca 480

acccttgcac gctacgaatg agtagtcttt ttggatattt tgatccatca tgcagctttg 540

a 541

<210> 155

<211> 2109

<212> DNA

<213> *Protochlorococcus marinus* MED4

<400> 155

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gaaatattaa gggctttcca attacgcttg gataaaactc ctgatgaagg attcacgtac 120

gagggttttaa ctcaaaggtc ggaattgctt cgccttactg cagatttgct tacagatcca 180

gatagtagaa gagattacga aaatttatta ctaaatggag catcagggtt agatttatct 240

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gaagctgac ttaccttggt agcggcttta acatctagag atgctgcaat acaagagcaa 420

gatcaaagat ctactcaaa tgctgcagat tttttacaag aaggcataca gcttcttcaa 480

agaatgggca aactagggga attacggaaa actcttgagg aggacttagt gtcgcttctt 540

ccgtatcgaa ttcttgattt gttaagtaga gatctaaatg attatgactc gcataaaaaa 600

ggtttaagta tgctggaaaa ttaataatc aaaagagggtg gattagaagg aaaaaataaa 660

tctgaatata atgattttct aaatcagcaa gaatttgaat ctttctttca acaaataaag 720

ccattcttga ctgttcagga tcagatagat ttatttttag aattacaaaa aaggggttca 780

agtgaagcag gatttttagc ttttttatct ttaacagcaa ttggttttgc aagaagaaaa 840

cctgcaaaat tattcgaaag tcgaaaaata ttaaaaaaac taaatttatc aggacttgac 900

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tatagggata ttgattttaa agaaatcgat ttagactctt ggtttgaaga tagagaaatc 1140

caagaattta ttgagcaaat agaaaagaag tcaaatagaa ctgtgtttta gtctgggcct 1200

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gaaaaaatat taaaaataga tggggaattg ataaatgaaa caactttcac tccttttttg 2040
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<210> 156
<211> 702
<212> PRT
<213> *Protochlorococcus marinus* MED4

<400> 156

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Ala Thr Ser Glu Glu Ile Leu Arg Ala Phe Gln Leu Arg Leu Asp Lys
20 25 30

Thr Pro Asp Glu Gly Phe Thr Tyr Glu Val Leu Thr Gln Arg Ser Glu
35 40 45

Leu Leu Arg Leu Thr Ala Asp Leu Leu Thr Asp Pro Asp Ser Arg Arg
50 55 60

Asp Tyr Glu Asn Leu Leu Leu Asn Gly Ala Ser Gly Leu Asp Leu Ser
65 70 75 80

Ser Asn Arg Glu Val Ala Gly Leu Ile Leu Leu Trp Glu Ser Gly Ser
85 90 95

Ser Lys Glu Ala Phe Lys Ile Thr Arg Lys Ala Leu Gln Pro Pro Gln
100 105 110

Thr Pro Ala Leu Gly Ser Ser Arg Glu Ala Asp Leu Thr Leu Leu Ala
115 120 125

Ala Leu Thr Ser Arg Asp Ala Ala Ile Gln Glu Gln Asp Gln Arg Ser
130 135 140

Tyr Ser Asn Ala Ala Asp Phe Leu Gln Glu Gly Ile Gln Leu Leu Gln
145 150 155 160

Arg Met Gly Lys Leu Gly Glu Leu Arg Lys Thr Leu Glu Glu Asp Leu
165 170 175

Val Ser Leu Leu Pro Tyr Arg Ile Leu Asp Leu Leu Ser Arg Asp Leu
180 185 190

Asn Asp Tyr Asp Ser His Lys Lys Gly Leu Ser Met Leu Glu Asn Leu
195 200 205

Ile Ile Lys Arg Gly Gly Leu Glu Gly Lys Asn Lys Ser Glu Tyr Asn
210 215 220

Asp Phe Leu Asn Gln Gln Glu Phe Glu Ser Phe Phe Gln Gln Ile Lys
225 230 235 240

Pro Phe Leu Thr Val Gln Asp Gln Ile Asp Leu Phe Leu Glu Leu Gln
245 250 255

Lys Arg Gly Ser Ser Glu Ala Gly Phe Leu Ala Phe Leu Ser Leu Thr
260 265 270

Ala Ile Gly Phe Ala Arg Arg Lys Pro Ala Lys Leu Phe Glu Ala Arg
275 280 285

Lys Ile Leu Lys Lys Leu Asn Leu Ser Gly Leu Asp Ser Met Pro Leu
290 295 300

Ile Gly Cys Leu Asp Leu Leu Leu Ala Asp Val Glu Gln Ser Ser Ala
305 310 315 320

Arg Phe Leu Ser Ser Ser Asp Glu Lys Leu Arg Asp Trp Leu Asn Asn
325 330 335

Tyr Pro Gly Glu Lys Leu Glu Ala Ile Cys Ile Phe Cys Lys Asn Trp
340 345 350

Leu Glu Asn Asp Val Leu Val Gly Tyr Arg Asp Ile Asp Leu Lys Glu
355 360 365

Ile Asp Leu Asp Ser Trp Phe Glu Asp Arg Glu Ile Gln Glu Phe Ile
370 375 380

Glu Gln Ile Glu Lys Lys Ser Asn Arg Thr Val Phe Lys Ser Gly Pro

385		390		395		400
Gln Asn Lys Pro	Ile Phe Gln Ala Gln Glu Ser Leu Lys Asp Ser Ser					
	405			410		415
Thr Gly Pro Asp	Leu Asn Ser Asp Asn Phe Glu Glu Gly Arg Leu Pro					
	420			425		430
Leu Pro Gly Gly	Val Arg Glu Asp Gly Gln Glu Val Ile Glu Glu Asn					
	435			440		445
Ile Tyr Thr Asp	Glu Ile Ile Lys Asn Lys Ser Ile Glu Phe Tyr Lys					
	450			455		460
Tyr Ala Ile Glu Lys	Ile Ala Glu Leu Lys Phe Val Phe Gly Glu Ala					
	465			470		480
Leu Glu Asn Tyr	Arg Ile Phe Asn Lys Ser Ser Tyr Leu Thr Tyr Leu					
	485			490		495
Tyr Ala Phe Leu	Ile Leu Phe Ala Phe Gly Leu Gly Val Gly Phe Val					
	500			505		510
Arg Asn Asn Leu Lys Lys	Pro Val Gln Glu Lys Glu Ile Ile Asp Asn					
	515			520		525
Ser Leu Ser Ile Asn Glu	Asn Lys Asn Val Phe Tyr Glu Gly Leu Asn					
	530			535		540
Gln Asp Asp Lys Lys	Lys Val Leu Asp Asn Ser Lys Ile Ile Leu Ser					
	545			550		555
Asp Asn Ala Glu Lys Val	Ile Phe Ser Gly Glu Glu Ile Lys Thr Ala					
	565			570		575
Ser Pro Ser Leu Glu Lys	Ile Glu Asn Leu Ile Asn Thr Trp Leu Val					
	580			585		590
Asn Lys Ser Lys Phe Leu	Ala Gly Lys Gly Glu Ile Asn Leu Ser Lys					
	595			600		605
Ile Val Gln Asp Asp	Leu Ile Asp Arg Leu Lys Lys Glu Arg Glu Leu					
	610			615		620
Asp Ile Gln Lys Gly	Ile Tyr Lys Asn Ile Asn Ala Asn Ile Glu Asn					
	625			630		635
						640

Ile Val Leu Leu Thr Gln Thr Ala Ser Arg Ile Ser Val Ser Val Asp
645 650 655

Leu Lys Tyr Ser Glu Lys Ile Leu Lys Ile Asp Gly Glu Leu Ile Asn
660 665 670

Glu Thr Thr Phe Thr Pro Phe Leu Lys Val Lys Tyr Ile Leu Gly Phe
675 680 685

Ser Asn Asn Ser Trp Lys Leu Val Asp Tyr Ile Ser Gly Val
690 695 700

<210> 157
<211> 1986
<212> DNA
<213> Protochlorococcus marinus MT9313

<400> 157
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aaataa 1986

<210> 158
<211> 661
<212> PRT
<213> *Protochlorococcus marinus* MT9313

<400> 158

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20 25 30

Cys Pro Asp Gln Gly Phe Thr His Glu Val Leu Ile Gln Arg Ala Glu
35 40 45

Leu Leu Arg Leu Ser Ala Asp Leu Leu Thr Asp Pro Pro Arg Arg Gln
50 55 60

Ala Tyr Glu Thr Ala Leu Leu Glu Leu Ser Arg Asp His Pro Gly Glu
65 70 75 80

Thr Ala Gly Leu Asp Val Ser Pro Ser Arg Glu Val Ala Gly Leu Ile
85 90 95

Leu Leu Phe Glu Ala Asn Ser Ser His Glu Val Phe His Leu Ala Ser
100 105 110

Gln Gly Leu Gln Pro Pro Gln Ser Pro Thr Leu Gly Ser Glu Arg Glu
 115 120 125

Ala Asp Leu Ala Leu Leu Leu Ala Leu Ala Cys Arg Ala Ala Ala Ala
 130 135 140

Glu Glu Gln Glu Gln Arg Arg Tyr Glu Ala Ala Ala Ser Leu Leu His
 145 150 155 160

Asp Gly Ile Gln Leu Leu Gln Arg Met Gly Lys Leu Ser Glu Glu Cys
 165 170 175

His Lys Leu Glu Asn Asp Leu Asp Ala Leu Leu Pro Tyr Arg Ile Leu
 180 185 190

Asp Leu Leu Ser Arg Asp Leu Gly Asp Gln Val Ser His Gln Glu Gly
 195 200 205

Leu Arg Leu Leu Asp Asn Phe Val Ser Gln Arg Gly Gly Leu Glu Gly
 210 215 220

Thr Ala Pro Ser Pro Ala Pro Gly Gly Leu Asp Gln Ser Glu Phe Asp
 225 230 235 240

Asn Phe Phe Lys Gln Ile Arg Lys Phe Leu Thr Val Gln Glu Gln Val
 245 250 255

Asp Leu Phe Leu Arg Trp Gln Gln Ala Gly Ser Ala Asp Ala Gly Phe
 260 265 270

Leu Gly Gly Leu Ala Leu Ala Ala Val Gly Phe Ser Arg Arg Lys Pro
 275 280 285

Glu Arg Val Gln Glu Ala Arg Gln His Leu Glu Arg Leu Gln Leu Asp
 290 295 300

Gly Cys Asp Pro Leu Pro Met Leu Gly Cys Leu Asp Leu Leu Leu Gly
 305 310 315 320

Asp Val Gly Arg Ala Gln Glu Arg Phe Leu Arg Ser Thr Asp Pro Arg
 325 330 335

Val Lys Asp Cys Leu Asn Ser His Pro Gly Asp Glu Leu Ala Ala Phe
 340 345 350

Cys Glu Tyr Cys Arg Ser Trp Leu Arg Gly Asp Val Leu Pro Gly Tyr

355					360					365					
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Arg	Asp	Val	Gln	Ala	Tyr	Val	Glu	Arg	Leu	Glu	Arg	Ser	Glu	Asn	Arg
385					390					395					400
Ala	Ser	Ser	Leu	Gly	Lys	Ala	Phe	Ser	Gly	Ser	Ser	Val	Lys	Gln	Pro
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Phe	Pro	Trp	Ala	Pro	Leu	Asp	Pro	Asp	Gly	Ile	Leu	Pro	Leu	Ser	Leu
			420					425					430		
Gly	Gly	Pro	Asp	Val	Gly	Gln	Pro	Ala	Ala	Asp	Gln	Ser	Ser	Asp	Glu
		435					440					445			
Phe	Ala	Ser	Asp	Gly	Met	Ala	Trp	Ile	Asp	Arg	Leu	Ala	Asp	Leu	Pro
	450					455					460				
Arg	Pro	Thr	Arg	Pro	Val	Leu	Ile	Gly	Ser	Val	Val	Phe	Ala	Ala	Leu
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Ile	Ala	Ala	Phe	Ala	Gly	Phe	Ser	Leu	Phe	Gly	Gln	Arg	Pro	Arg	Thr
			485						490					495	
Ser	Val	Ser	Thr	Ala	Ala	Asp	Gln	Pro	Gln	Val	Thr	Ala	Pro	Pro	Thr
			500					505					510		
Ala	Thr	Leu	Gln	Glu	Glu	Val	Leu	Met	Pro	Gln	Val	Pro	Val	Ser	Ala
		515					520					525			
Val	Val	Glu	Pro	Leu	Thr	Leu	Glu	Gln	Pro	Asn	Glu	Ala	Gln	Leu	Lys
	530					535					540				
Gly	Leu	Leu	Gln	Ala	Trp	Leu	Ser	Asn	Lys	Ala	Val	Val	Leu	Ala	Gly
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Gly	Lys	Ser	Asp	Ala	Leu	Pro	Glu	Val	Ala	Arg	Asp	Pro	Leu	Val	Gln
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Arg	Val	Ala	Gln	Glu	Arg	Ala	Arg	Asp	Ala	Ala	Leu	Ala	Gln	Thr	Gln
			580					585					590		
Lys	Val	Val	Ala	Ser	Ile	Ser	Ser	Val	Glu	Val	Val	Ser	Arg	Thr	Pro
	595					600						605			

Gln Arg Ile Glu Leu Asn Ala Val Val Thr Tyr Arg Asp Gln Arg Val
610 615 620

Asp Ala Ala Gly Lys Val Val Asp Gln Thr Pro Gln Lys Asp Leu Ser
625 630 635 640

Val Thr Tyr Ile Leu Gly Arg Asp Pro Asp Arg Trp Arg Leu His Glu
645 650 655

Tyr Ile Ser Gly Lys
660

<210> 159
<211> 2151
<212> DNA
<213> Synechococcus PCC7002

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ttggccattg agggccgcaa ccggattatc gagcaagcct ttgaggtgtt atcccaaaca 180
gaaaccgcg ccgtctacga ccatgagctg tcgggcaata tgtttcgttc cctcgtcccc 240
agccgtccga aactgccttt tcccgatcgc ccctccagtg acacagagtt agaagccctg 300
acagcccacc aaccaaccat tgacatcgcg gaaaaagatt tactgggggg actgctgtta 360
ctcctcgacc tgggggagta cgaattagtg ctgaagtggg ctgccccta cctcaagggc 420
aaaggcaagc tgggtcaagga agggaaattt ggggccgtcg aaatcgtcga gcaagaacta 480
cggctttgtt tggccctggc ccactgggaa ttgagccggg aacagtggct ccaacaacat 540
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tttgagacc tccaacagga aattcaaggg gatctcaatc gcctcagacc ctatcaagtt 660
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 gcgaatgggg aacgcgatcc cggccagtcc tatgattctg acctgcgtgt ccgctacagc 2100
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<210> 160
 <211> 716
 <212> PRT
 <213> Synechococcus PCC7002

<400> 160

Met Arg Ile Pro Leu Asp Tyr Tyr Arg Ile Leu Cys Val Pro Ala Lys
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Ala Thr Thr Ala Gln Ile Thr Gln Ala Tyr Arg Asp Arg Leu Ser Gln
 20 25 30

Phe Pro Arg Arg Glu His Asn Ala Leu Ala Ile Glu Ala Arg Asn Arg
 35 40 45

Ile Ile Glu Gln Ala Phe Glu Val Leu Ser Gln Thr Glu Thr Arg Ala
 50 55 60

Val Tyr Asp His Glu Leu Ser Gly Asn Met Phe Arg Ser Leu Val Pro
 65 70 75 80

Ser Arg Pro Lys Leu Pro Phe Pro Asp Arg Pro Ser Ser Asp Thr Glu
 85 90 95

Leu Glu Ala Leu Thr Ala His Gln Pro Thr Ile Asp Ile Ala Glu Lys
 100 105 110
 Asp Leu Leu Gly Gly Leu Leu Leu Leu Leu Asp Leu Gly Glu Tyr Glu
 115 120 125
 Leu Val Leu Lys Trp Ala Ala Pro Tyr Leu Lys Gly Lys Gly Lys Leu
 130 135 140
 Val Lys Glu Gly Lys Phe Gly Ala Val Glu Ile Val Glu Gln Glu Leu
 145 150 155 160
 Arg Leu Cys Leu Ala Leu Ala His Trp Glu Leu Ser Arg Glu Gln Trp
 165 170 175
 Leu Gln Gln His Tyr Glu Gln Ala Ala Leu Ser Gly Gln Lys Ser Gln
 180 185 190
 Glu Leu Leu Val Asp Val Ala Gln Phe Ala Asp Leu Gln Gln Glu Ile
 195 200 205
 Gln Gly Asp Leu Asn Arg Leu Arg Pro Tyr Gln Val Leu Glu Leu Leu
 210 215 220
 Ala Leu Pro Glu Ser Glu Thr Gln Glu Arg Gln Arg Gly Leu Gln Leu
 225 230 235 240
 Leu Gln Glu Met Leu Ser Ala Arg Val Gly Ile Asp Gly Gln Gly Asp
 245 250 255
 Asp Gln Ser Gly Leu Ser Ile Asp Asp Phe Leu Arg Phe Ile Gln Gln
 260 265 270
 Leu Arg Ser Tyr Leu Thr Val Gln Glu Gln Leu Asp Leu Phe Val Ala
 275 280 285
 Glu Ser Lys Arg Pro Ser Ala Ala Ala Ala Tyr Leu Ala Val Tyr Ala
 290 295 300
 Leu Leu Ala Ala Gly Phe Ser Gln Arg Lys Pro Asp Leu Val Val Gln
 305 310 315 320
 Ala Gln Thr Leu Leu Lys Arg Leu Gly Lys Arg Gln Asp Val Phe Leu
 325 330 335
 Glu Gln Ser Ile Cys Ala Leu Leu Leu Gly Gln Pro Ser Glu Ala Asn

340	345	350
Gln Leu Leu Glu Gln Ser Gln Glu Gln Glu Ala Ile Ala Tyr Ile Gln 355 360 365		
Glu Gln Ser Glu Gly Ala Pro Asp Leu Leu Pro Gly Leu Cys Leu Tyr 370 375 380		
Gly Glu Gln Trp Leu Lys Thr Glu Val Phe Ser His Phe Arg Asp Leu 385 390 395 400		
Arg Gln Arg Leu Glu Asp Gly Ser Val Ser Leu Thr Ala Tyr Phe Ala 405 410 415		
Asp Pro Glu Val Gln Gln Tyr Leu Asp Asp Leu Leu Thr Glu Ala Val 420 425 430		
Pro Thr Pro Thr Pro His Pro Asp Thr Glu Ser Thr Ala Ala Pro Ser 435 440 445		
Glu Lys Pro Pro Glu Thr Leu Gln Ser Glu Thr Gly Val Ser Pro His 450 455 460		
Pro Ser Arg Pro Ala Lys Val Asp Ser Phe Glu Asp Leu Val Thr Gln 465 470 475 480		
Thr Pro Ala Thr Val Pro Pro Ala Pro Pro Ser Pro Gly Val Ala Pro 485 490 495		
Val Thr Ala Ala Leu Asn Pro Asp Pro Glu Ala Ser Ser Ala Ser Ser 500 505 510		
Lys Ser Val Ser Ser Lys Lys Ser Ile Gly Pro Trp Gly Ala Ile Ala 515 520 525		
Ala Ile Val Gly Ser Val Leu Leu Val Val Gly Leu Val Arg Ile Leu 530 535 540		
Ser Gly Leu Thr Thr Gln Glu Pro Leu Gln Val Thr Leu Asn Gly Glu 545 550 555 560		
Pro Pro Leu Thr Ile Pro Ser Leu Asp Thr Ala Glu Ala Asn Asn Asn 565 570 575		
Pro Glu Asn Gly Ala Thr Asp Thr Thr Thr Pro Ala Leu Asn Glu 580 585 590		

Ala Ile Ala Ala Glu Val Ile Gln Thr Trp Phe Glu Ser Lys Ala Arg
595 600 605

Ala Phe Gly Gln Asp Arg Asp Leu Ala Ala Leu Glu Asn Ile Leu Ala
610 615 620

Glu Pro Ser Leu Ser Arg Trp Arg Ser Ser Ala Gln Ala Val Arg Ser
625 630 635 640

Ala Gly Thr Tyr Arg Thr Tyr Asp His Ser Leu Thr Ile Glu Thr Val
645 650 655

Ser Phe Asn Pro Asp Gln Pro Asn Val Ala Thr Val Glu Ala Gln Val
660 665 670

Gln Glu Lys Ala Asp Tyr Tyr Arg Ala Asn Gly Glu Arg Asp Pro Gly
675 680 685

Gln Ser Tyr Asp Ser Asp Leu Arg Val Arg Tyr Ser Leu Val Arg Gln
690 695 700

Gly Asp Arg Trp Leu Ile Arg Ser Ser Gln Thr Leu
705 710 715

<210> 161
<211> 2469
<212> DNA
<213> Synechococcus PCC7942

<400> 161
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gcgagtaacc gatcgctggg ataagagttg gtgcttcttg ctctcaagaa tagggtttcc 180
cgtcgcgtat tcccgatcac atccccctgt gtctgctacg gagataacgc cgatcactca 240
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<210> 162

<211> 631
 <212> PRT
 <213> Synechococcus PCC7942

<400> 162

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Ala Ser Ala Asp Lys Leu Ala Glu Ser Tyr Arg Asp Arg Leu Asn Gln
 20 25 30

Ser Pro Ser His Glu Phe Ser Glu Leu Ala Leu Gln Ala Arg Arg Gln
 35 40 45

Leu Leu Glu Ala Ala Ile Ala Glu Leu Ser Asp Pro Glu Gln Arg Asp
 50 55 60

Arg Tyr Asp Arg Arg Phe Phe Gln Gly Gly Leu Glu Ala Ile Glu Pro
 65 70 75 80

Ser Leu Glu Leu Glu Asp Trp Gln Arg Ile Gly Ala Leu Leu Ile Leu
 85 90 95

Leu Glu Leu Gly Glu Tyr Asp Arg Val Ser Gln Leu Ala Glu Glu Leu
 100 105 110

Leu Pro Asp Tyr Asp Ala Ser Ala Glu Val Arg Asp Gln Phe Ala Arg
 115 120 125

Gly Asp Ile Ala Leu Ala Ile Ala Leu Ser Gln Gln Ser Leu Gly Arg
 130 135 140

Glu Cys Arg Gln Gln Gly Leu Tyr Glu Gln Ala Ala Gln His Phe Gly
 145 150 155 160

Arg Ser Gln Ser Ala Leu Ala Asp His Gln Arg Phe Pro Glu Leu Ser
 165 170 175

Arg Thr Leu His Gln Glu Gln Gly Gln Leu Arg Pro Tyr Arg Ile Leu
 180 185 190

Glu Arg Leu Ala Gln Pro Leu Thr Ala Asp Ser Asp Arg Gln Gln Gly
 195 200 205

Leu Leu Leu Leu Gln Ala Met Leu Asp Asp Arg Gln Gly Ile Glu Gly
 210 215 220

Pro Gly Asp Asp Gly Ser Gly Leu Thr Leu Asp Asn Phe Leu Met Phe
225 230 235 240

Leu Gln Gln Ile Arg Gly Tyr Leu Thr Leu Ala Glu Gln Gln Leu Leu
245 250 255

Phe Glu Ser Glu Ala Arg Arg Pro Ser Pro Ala Ala Ser Phe Phe Ala
260 265 270

Cys Tyr Thr Leu Ile Ala Arg Gly Phe Cys Asp His Gln Pro Ser Leu
275 280 285

Ile His Arg Ala Ser Leu Leu Leu His Glu Leu Lys Ser Arg Met Asp
290 295 300

Val His Ile Glu Gln Ala Ile Ala Ser Leu Leu Leu Gly Gln Pro Glu
305 310 315 320

Glu Ala Glu Ala Leu Leu Val Gln Ser Gln Asp Glu Glu Thr Leu Ser
325 330 335

Gln Ile Arg Ala Leu Ala Gln Gly Glu Ala Leu Ile Val Gly Leu Cys
340 345 350

Arg Phe Thr Glu Thr Trp Leu Ala Thr Lys Val Phe Pro Asp Phe Arg
355 360 365

Asp Leu Lys Glu Arg Thr Ala Pro Leu Gln Pro Tyr Phe Asp Asp Pro
370 375 380

Asp Val Gln Thr Tyr Leu Asp Ala Ile Val Glu Leu Pro Ser Asp Leu
385 390 395 400

Met Pro Thr Pro Leu Pro Val Glu Pro Leu Glu Val Arg Ser Ser Leu
405 410 415

Leu Ala Lys Glu Leu Pro Thr Pro Ala Thr Pro Gly Val Ala Pro Pro
420 425 430

Pro Arg Arg Arg Arg Asp Arg Ser Glu Arg Pro Ala Arg Thr Ala
435 440 445

Lys Arg Leu Pro Leu Pro Trp Ile Gly Leu Gly Val Val Val Val Leu
450 455 460

Gly Gly Gly Thr Gly Val Trp Ala Trp Arg Ser Arg Ser Asn Ser Thr
465 470 475 480

Pro Pro Thr Pro Pro Pro Val Val Gln Thr Leu Pro Glu Ala Val Pro
485 490 495

Ala Pro Ser Pro Ala Pro Val Thr Val Ala Leu Asp Arg Ala Gln Ala
500 505 510

Glu Thr Val Leu Gln Asn Trp Leu Ala Ala Lys Ala Ala Ala Leu Gly
515 520 525

Pro Gln Tyr Asp Arg Asp Arg Leu Ala Thr Val Leu Thr Gly Glu Val
530 535 540

Leu Gln Thr Trp Gln Gly Phe Ser Ser Gln Gln Ala Asn Thr Gln Leu
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Thr Ser Gln Phe Asp His Lys Leu Thr Val Asp Ser Val Gln Leu Ser
565 570 575

Asp Gly Asp Gln Arg Ala Val Val Gln Ala Lys Val Asp Glu Val Glu
580 585 590

Gln Val Tyr Arg Gly Asp Gln Leu Leu Glu Thr Arg Arg Asp Leu Gly
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Ala Ser Ile Ser Leu Val Arg
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Ser Gln Ala Ala Ile Ala Ser Arg Lys Gln Leu Ile Glu Glu Ala Tyr
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Val Val Leu Ser Asp Pro Lys Glu Arg Ser Ser Tyr Asp Gln Leu Tyr
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Leu Ala His Ala Tyr Asp Pro Asp Asn Ala Ala Thr Thr Lys Val Ala
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Val Glu Asn Arg Gly Asp Ser Asn Asn Gly His Phe Asp Val Gln Ser
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Leu Gln Glu Leu Gly Glu Tyr Glu Leu Val Leu Lys Leu Gly Arg Asn
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Tyr Leu Gly Asn Gln Asn Gly Thr Ala Ser Thr Arg Asn Gly Asn His
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Arg Thr Pro Glu Glu Phe Leu Asp Ser Ser Glu Arg Pro Asp Ile Leu
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Gln Gly His Tyr Glu Asn Ala Ala Leu Ser Leu Glu Thr Gly Gln Glu
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Val Leu Phe Ser Glu Gly Ile Phe Pro Ser Val Gln Ala Glu Ile Gln
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Ala Asp Leu Tyr Lys Leu Arg Pro Tyr Arg Ile Leu Glu Leu Leu Ala
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Leu Pro Gln Glu Lys Thr Ile Glu Arg His Gln Gly Leu Asp Leu Leu
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Gln Ser Ile Leu Asp Asp Arg Gly Gly Ile Asp Gly Thr Gly Asn Asp
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Gln Ser Gly Leu Asn Ile Asp Asp Phe Leu Arg Phe Ile Gln Gln Leu
 275 280 285

Arg His His Leu Thr Val Ala Glu Gln His Lys Leu Phe Asp Gly Glu
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Ser Lys Arg Pro Ser Ala Val Ala Thr Tyr Leu Ala Val Tyr Ala Ser
 305 310 315 320

Ile Ala Arg Gly Phe Thr Gln Arg Gln Pro Ala Leu Ile Arg His Ala
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Lys Gln Ile Leu Met Arg Leu Ser Lys Arg Gln Asp Val His Leu Glu
 340 345 350

Gln Ser Leu Cys Ala Leu Leu Leu Gly Gln Thr Glu Glu Ala Thr Arg
 355 360 365

Val Leu Glu Leu Ser Gln Glu Tyr Glu Ala Leu Ala Leu Ile Arg Glu
 370 375 380

Lys Ser Gln Asp Ser Pro Asp Leu Leu Pro Gly Leu Cys Leu Tyr Ala
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Glu Gln Trp Leu Gln Asn Glu Val Phe Pro His Phe Arg Asp Leu Ser
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Arg Gln Gln Ala Ser Leu Lys Asp Tyr Phe Ala Asn Gln Gln Val Gln
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Ala Tyr Leu Glu Ala Leu Pro Asn Asp Ala Glu Thr Thr Asn Glu Trp
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Ala Val Ile Asn Arg Gln Ser Phe Ser Gln Pro Arg Gly Asn Ser Tyr
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Ser Gly Gly Thr Pro Val Ala Lys Arg Pro Val Gly Lys Ala Asn Arg
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Pro Gly Glu Ala Ser Thr Arg Pro Val Pro Gln Arg Ser His Pro Ser
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Glu Val Asn Arg Gln Phe His Gln Asn Arg Thr Pro Asp Pro Glu Leu
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Pro Glu Thr Ser Asn His Arg Arg Pro Glu Ser Ser Asn Phe Thr Thr
515 520 525

Ala Arg Glu Asn Ile Ser Thr Thr Asp Ala Tyr Thr Asp Asn Tyr Pro
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Pro Glu Ile Pro Val Glu Arg Ala Ser Arg Pro Val Gln Pro Gly Val
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Ser Gly Tyr Thr Gln Ser Thr Pro Pro Arg Gln Thr Pro Lys Arg Arg
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Arg Arg Lys Lys Pro Gln Ala Val Val Asn Arg Gly His Ser Ile His
580 585 590

Gln Gln Arg Gln Pro Ser Pro Ser Thr Leu Gly Arg Lys Thr Arg Leu
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Leu Trp Ile Val Leu Gly Ser Leu Gly Gly Ile Leu Leu Phe Trp Leu
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Ile Val Ser Thr Thr Phe Gly Trp Leu Lys Asn Val Phe Phe Pro Ala
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Pro Ser Leu Gln Gly Glu Gln Leu Ser Ile Gln Ile Ser Gln Pro Pro
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Leu Glu Ile Pro Asp Lys Asn Ala Gln Ile Gln Ser Pro Glu Val Ser
660 665 670

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Lys Ala Ser Ala Leu Gly Ala Glu His Lys Ile Glu Ser Leu Asn Glu
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Leu Gln Glu Leu Gly Glu Tyr Glu Leu Val Leu Lys Leu Gly Arg Asn
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Tyr Leu Gly Asn Gln Asn Gly Thr Ala Ser Thr Arg Asn Gly Asn His
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Arg Thr Pro Glu Glu Phe Leu Asp Ser Ser Glu Arg Pro Asp Ile Leu
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Leu Thr Val Ala Leu Ala Ser Leu Glu Leu Gly Arg Glu Gln Trp Gln
 180 185 190

Gln Gly His Tyr Glu Asn Ala Ala Leu Ser Leu Glu Thr Gly Gln Glu
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Val Leu Phe Ser Glu Gly Ile Phe Pro Ser Val Gln Ala Glu Ile Gln
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Ala Asp Leu Tyr Lys Leu Arg Pro Tyr Arg Ile Leu Glu Leu Leu Ala
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Leu Pro Gln Glu Lys Thr Ile Glu Arg His Gln Gly Leu Asp Leu Leu
 245 250 255

Gln Ser Ile Leu Asp Asp Arg Gly Gly Ile Asp Gly Thr Gly Asn Asp
 260 265 270

Gln Ser Gly Leu Asn Ile Asp Asp Phe Leu Arg Phe Ile Gln Gln Leu
 275 280 285

Arg His His Leu Thr Val Ala Glu Gln His Lys Leu Phe Asp Gly Glu
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Ser Lys Arg Pro Ser Ala Val Ala Thr Tyr Leu Ala Val Tyr Ala Ser
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Ile Ala Arg Gly Phe Thr Gln Arg Gln Pro Ala Leu Ile Arg His Ala
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Lys Gln Ile Leu Met Arg Leu Ser Lys Arg Gln Asp Val His Leu Glu
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Gln Ser Leu Cys Ala Leu Leu Leu Gly Gln Thr Glu Glu Ala Thr Arg
 355 360 365

Val Leu Glu Leu Ser Gln Glu Tyr Glu Ala Leu Ala Leu Ile Arg Glu
 370 375 380

Lys Ser Gln Asp Ser Pro Asp Leu Leu Pro Gly Leu Cys Leu Tyr Ala
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Glu Gln Trp Leu Gln Asn Glu Val Phe Pro His Phe Arg Asp Leu Ser
405 410 415

Arg Gln Gln Ala Ser Leu Lys Asp Tyr Phe Ala Asn Gln Gln Val Gln
420 425 430

Ala Tyr Leu Glu Ala Leu Pro Asn Asp Ala Glu Thr Thr Asn Glu Trp
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Ala Val Ile Asn Arg Gln Ser Phe Ser Gln Pro Arg Gly Asn Ser Tyr
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Ser Gly Gly Thr Pro Val Ala Lys Arg Pro Val Gly Lys Ala Asn Arg
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Pro Gly Glu Ala Ser Thr Arg Pro Val Pro Gln Arg Ser His Pro Ser
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Glu Val Asn Arg Gln Phe His Gln Asn Arg Thr Pro Asp Pro Glu Leu
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Pro Glu Thr Ser Asn His Arg Arg Pro Glu Ser Ser Asn Phe Thr Thr
515 520 525

Ala Arg Glu Asn Ile Ser Thr Thr Asp Ala Tyr Thr Asp Asn Tyr Pro
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Pro Glu Ile Pro Val Glu Arg Ala Ser Arg Pro Val Gln Pro Gly Val
545 550 555 560

Ser Gly Tyr Thr Gln Ser Thr Pro Pro Arg Gln Thr Pro Lys Arg Arg
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Arg Arg Lys Lys Pro Gln Ala Val Val Asn Arg Gly His Ser Ile His
580 585 590

Gln Gln Arg Gln Pro Ser Pro Ser Thr Leu Gly Arg Lys Thr Arg Leu
595 600 605

Leu Trp Ile Val Leu Gly Ser Leu Gly Gly Ile Leu Leu Phe Trp Leu
610 615 620

Ile Val Ser Thr Thr Phe Gly Trp Leu Lys Asn Val Phe Phe Pro Ala

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Lys Ala Ser Ala Leu Gly Ala Glu His Lys Ile Glu Ser Leu Asn Glu						
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Ala Thr Val Arg Glu Leu Thr Gln Phe Tyr Glu Asn Gly Gln Lys Gly						
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Lys Ser Ser Asp Glu Arg Leu Arg Val Arg Tyr Glu Leu Ile Arg Gln						
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cagagtcttg gtatagaaat tacccaagac gaattagttg gcgctttatt aattttgcaa	360
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<212> PRT

<213> Nostoc punctiforme

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Thr Tyr Asp Gln Leu Tyr Leu Ala His Ala Tyr Asp Pro Asp Asn Leu
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Ala Ala Ala Ala Val Ala Gln Glu Asn Arg Thr Glu Ser Thr Lys Arg
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Gly Ser Asp Thr Gln Ser Leu Gly Ile Glu Ile Thr Gln Asp Glu Leu
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Val Gly Ala Leu Leu Ile Leu Gln Glu Leu Gly Glu Tyr Glu Leu Val
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Leu Lys Leu Gly Arg Pro Tyr Leu Val Asn Lys Asn Ser Ala Thr Ser
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Ser Arg Lys Ser Asn Asn Leu Ala Asp Glu Glu Ile Tyr Glu Ser Ala
145 150 155 160

Glu His Pro Asp Val Val Leu Thr Val Ala Leu Ala Cys Leu Glu Leu
165 170 175

Gly Arg Glu Gln Trp Gln Gln Gly His Tyr Glu Asn Ala Ala Ile Ser
180 185 190

Leu Glu Thr Gly Gln Glu Leu Leu Val Arg Glu Gly Leu Phe Ser Ser
195 200 205

Ile Gln Ala Glu Ile Gln Ala Asp Leu Tyr Lys Leu Arg Pro Tyr Arg
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 Ala Lys Ala Lys Asn Thr His Phe His Asn Asn Ser Thr Lys Thr Ser
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Pro Thr Lys Glu Thr Ser Glu Tyr Pro Asn Phe Ser Pro Pro Met Trp
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Ser Arg Gly Thr Asn Gln His Leu Asn Gly Ser Ala Lys Ser Ala Ala
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Ser Gly His Asn Gln Lys Arg Arg Arg Arg Lys Pro Thr Pro Ser Ala
 530 535 540

Ser Arg Glu Arg Ile Pro Asp Asn Arg Pro His Ser Arg Arg Pro Arg
 545 550 555 560

Arg Arg Arg Thr Phe Ala Asn Thr Ile Glu Gly Lys Thr Arg Leu Val
 565 570 575

Trp Arg Val Phe Ile Ser Leu Val Ser Ile Leu Val Phe Trp Val Leu
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Ala Thr Thr Thr Phe Gly Trp Leu Lys Asn Leu Phe Phe Pro Gln Pro
 595 600 605

Ser Pro Pro Asp Leu Gln Leu Phe Val Gln Ile Asn Gln Pro Pro Leu
 610 615 620

Pro Ile Pro Asp Pro Asn Arg Lys Pro Glu Ser Glu Glu Gly Pro Leu
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Thr Asn Ala Glu Ala Glu Glu Val Ile His Thr Trp Leu Ser Thr Lys
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Ala Ala Ala Leu Gly Pro Asn His Glu Ile Asn Asn Leu Glu Gln Ile
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 675 680 685

Lys Leu Asp Asn Arg Tyr Arg Lys Phe Asp His Ser Leu Lys Ile Glu
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Ser Val Glu Lys Ile Gly Leu Phe Ala Asp Arg Ala Ala Val Glu Ala

705

710

715

720

Thr Val Lys Glu Val Thr Gln Leu Tyr Glu Asn Asn Gln Phe Lys Asn
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<211> 2145

<212> DNA

<213> Synechocystis PCC6803

<400> 168

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 ctcccttgccc aacaacgggg tcgggcccga cgggatcaag cccaaaagggt ctatcaccaa 1920
 tacgaacaca agttgcagat tttagcctat caagttaacc cccaagacc caaccgagcc 1980
 accgttactg cccgggtaga agaaattagc cagcccttta ccctaggtaa tcaacagcag 2040
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<210> 169
 <211> 714
 <212> PRT
 <213> Synechocystis PCC6803
 <400> 169

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Ser Gly Gly Glu Thr Ile Glu Gln Ala Tyr Gln Asp Arg Leu Leu Gln
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Leu Pro Arg Arg Glu Phe Ser Asp Ala Ala Val Thr Leu Arg Asn Gln
 35 40 45

Leu Leu Ala Ile Ala Tyr Glu Thr Leu Arg Asp Pro Glu Lys Arg Gln
 50 55 60

Ala Tyr Asp Gln Glu Trp Trp Gly Ala Met Asp Glu Ala Leu Gly Glu
 65 70 75 80

Ala Leu Pro Leu Thr Thr Pro Glu Leu Glu Cys Ser Pro Glu Gln Glu
 85 90 95

Ile Gly Ala Leu Leu Ile Leu Leu Asp Leu Gly Glu Tyr Glu Leu Val
100 105 110

Val Lys Tyr Gly Glu Pro Val Leu His Asp Pro Asn Pro Pro Ala Gly
115 120 125

Gly Leu Pro Gln Asp Tyr Leu Leu Ser Val Ile Leu Ala His Trp Glu
130 135 140

Leu Ser Arg Glu Arg Trp Gln Gln Gln Gln Tyr Glu Phe Ala Ala Thr
145 150 155 160

Ala Ser Leu Lys Ala Leu Ala Arg Leu Gln Gln Asp Asn Asp Phe Pro
165 170 175

----- Ala Leu Glu Ala Glu Ile Arg Gln Glu Leu Tyr Arg Leu Arg Pro Tyr -----
180 185 190

Arg Ile Leu Glu Leu Leu Ala Lys Glu Gly Gln Gly Glu Glu Gln Arg
195 200 205

Gln Gln Gly Leu Ala Leu Leu Gln Ala Met Val Gln Asp Arg Gly Gly
210 215 220

Ile Glu Gly Lys Gly Glu Asp Tyr Ser Gly Leu Gly Asn Asp Asp Phe
225 230 235 240

Leu Lys Phe Ile His Gln Leu Arg Cys His Leu Thr Val Ala Glu Gln
245 250 255

Asn Ala Leu Phe Leu Pro Glu Ser Gln Arg Pro Ser Leu Val Ala Ser
260 265 270

Tyr Leu Ala Val His Ser Leu Met Ala Glu Gly Val Lys Glu Gln Asp
275 280 285

Pro Met Ala Ile Val Glu Ala Lys Ser Leu Ile Ile Gln Leu Glu Asn
290 295 300

Cys Gln Asp Leu Ala Leu Glu Lys Val Ile Cys Glu Leu Leu Leu Gly
305 310 315 320

Gln Thr Glu Val Val Leu Ala Ala Ile Asp Gln Gly Asp Pro Lys Ile
325 330 335

Val Ala Gly Leu Glu Ser Lys Leu Ala Thr Gly Glu Asp Pro Leu Thr
340 345 350

Ala Phe Tyr Thr Phe Thr Glu Gln Trp Leu Glu Glu Glu Ile Val Pro
355 360 365

Tyr Phe Arg Asp Leu Ser Pro Glu Thr Leu Ser Pro Lys Ala Tyr Phe
370 375 380

Asn Asn Pro Ser Val Gln Gln Tyr Leu Glu Gln Leu Glu Pro Asp Ser
385 390 395 400

Phe Thr Thr Asp Asn Ser Phe Ala Ser Pro Ala Leu Leu Ser Thr Ala
405 410 415

Thr Glu Ser Glu Thr Pro Met Val His Ser Ser Ala Ala Leu Pro Asp
420 425 430

Arg Pro Leu Thr Ser Thr Val Pro Ser Arg Arg Gly Arg Ser Pro Arg
435 440 445

Arg Ser Arg Asp Asp Val Phe Pro Ser Ala Asp Asn Ser Ser Gly Leu
450 455 460

Ala Val Thr Thr Leu Ser Pro Ala Ile Ala Tyr Asp Thr His Ser Leu
465 470 475 480

Gly Thr Asn Gly Ile Gly Gly Asp Ser Thr Ser Asn Gly Phe Ser Ser
485 490 495

Asn Ser Ala Pro Glu Ser Thr Ser Lys His Lys Ser Pro Arg Arg Arg
500 505 510

Lys Lys Arg Val Thr Ile Lys Pro Val Arg Phe Gly Ile Phe Leu Leu
515 520 525

Cys Leu Ala Gly Ile Val Gly Gly Ala Thr Ala Leu Ile Ile Asn Arg
530 535 540

Thr Gly Asp Pro Leu Gly Gly Leu Leu Glu Asp Pro Leu Asp Val Phe
545 550 555 560

Leu Asp Gln Pro Ser Glu Phe Ile Pro Asp Glu Ala Thr Ser Arg Asn
565 570 575

Leu Ile Leu Ser Gln Pro Asn Phe Asn Gln Gln Val Gly Gln Met Val
580 585 590

Val Gln Gly Trp Leu Asp Ser Lys Lys Leu Ala Phe Gly Gln Asn Tyr

595					600					605					
Asp	Val	Gly	Ala	Leu	Gln	Ser	Val	Leu	Ala	Pro	Asn	Leu	Leu	Ala	Gln
610						615					620				
Gln	Arg	Gly	Arg	Ala	Gln	Arg	Asp	Gln	Ala	Gln	Lys	Val	Tyr	His	Gln
625						630					635				640
Tyr	Glu	His	Lys	Leu	Gln	Ile	Leu	Ala	Tyr	Gln	Val	Asn	Pro	Gln	Asp
				645					650					655	
Pro	Asn	Arg	Ala	Thr	Val	Thr	Ala	Arg	Val	Glu	Glu	Ile	Ser	Gln	Pro
			660					665						670	
Phe	Thr	Leu	Gly	Asn	Gln	Gln	Gln	Lys	Gly	Ser	Ala	Thr	Lys	Asp	Asp
		675					680					685			
Leu	Thr	Val	Arg	Tyr	Gln	Leu	Val	Arg	His	Gln	Gly	Val	Trp	Lys	Ile
	690					695					700				
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<213> Synechocystis PCC6803															
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1				5					10					15	
Ser	Gly	Gly	Glu	Thr	Ile	Glu	Gln	Ala	Tyr	Gln	Asp	Arg	Leu	Leu	Gln
			20					25					30		
Leu	Pro	Arg	Arg	Glu	Phe	Ser	Asp	Ala	Ala	Val	Thr	Leu	Arg	Asn	Gln
			35				40					45			
Leu	Leu	Ala	Ile	Ala	Tyr	Glu	Thr	Leu	Arg	Asp	Pro	Glu	Lys	Arg	Gln
	50					55					60				
Ala	Tyr	Asp	Gln	Glu	Trp	Trp	Gly	Ala	Met	Asp	Glu	Ala	Leu	Gly	Glu
65						70					75				80
Ala	Leu	Pro	Leu	Thr	Thr	Pro	Glu	Leu	Glu	Cys	Ser	Pro	Glu	Gln	Glu
				85				90						95	

Ile Gly Ala Leu Leu Ile Leu Leu Asp Leu Gly Glu Tyr Glu Leu Val
100 105 110

Val Lys Tyr Gly Glu Pro Val Leu His Asp Pro Asn Pro Pro Ala Gly
115 120 125

Gly Leu Pro Gln Asp Tyr Leu Leu Ser Val Ile Leu Ala His Trp Glu
130 135 140

Leu Ser Arg Glu Arg Trp Gln Gln Gln Gln Tyr Glu Phe Ala Ala Thr
145 150 155 160

Ala Ser Leu Lys Ala Leu Ala Arg Leu Gln Gln Asp Asn Asp Phe Pro
165 170 175

Ala Leu Glu Ala Glu Ile Arg Gln Glu Leu Tyr Arg Leu Arg Pro Tyr
180 185 190

Arg Ile Leu Glu Leu Leu Ala Lys Glu Gly Gln Gly Glu Glu Gln Arg
195 200 205

Gln Gln Gly Leu Ala Leu Leu Gln Ala Met Val Gln Asp Arg Gly Gly
210 215 220

Ile Glu Gly Lys Gly Glu Asp Tyr Ser Gly Leu Gly Asn Asp Asp Phe
225 230 235 240

Leu Lys Phe Ile His Gln Leu Arg Cys His Leu Thr Val Ala Glu Gln
245 250 255

Asn Ala Leu Phe Leu Pro Glu Ser Gln Arg Pro Ser Leu Val Ala Ser
260 265 270

Tyr Leu Ala Val His Ser Leu Met Ala Glu Gly Val Lys Glu Gln Asp
275 280 285

Pro Met Ala Ile Val Glu Ala Lys Ser Leu Ile Ile Gln Leu Glu Asn
290 295 300

Cys Gln Asp Leu Ala Leu Glu Lys Val Ile Cys Glu Leu Leu Leu Gly
305 310 315 320

Gln Thr Glu Val Val Leu Ala Ala Ile Asp Gln Gly Asp Pro Lys Ile
325 330 335

Val Ala Gly Leu Glu Ser Lys Leu Ala Thr Gly Glu Asp Pro Leu Thr
340 345 350

Ala Phe Tyr Thr Phe Thr Glu Gln Trp Leu Glu Glu Glu Ile Val Pro
355 360 365

Tyr Phe Arg Asp Leu Ser Pro Glu Thr Leu Ser Pro Lys Ala Tyr Phe
370 375 380

Asn Asn Pro Ser Val Gln Gln Tyr Leu Glu Gln Leu Glu Pro Asp Ser
385 390 395 400

Phe Thr Thr Asp Asn Ser Phe Ala Ser Pro Ala Leu Leu Ser Thr Ala
405 410 415

Thr Glu Ser Glu Thr Pro Met Val His Ser Ser Ala Ala Leu Pro Asp
420 425 430

Arg Pro Leu Thr Ser Thr Val Pro Ser Arg Arg Gly Arg Ser Pro Arg
435 440 445

Arg Ser Arg Asp Asp Val Phe Pro Ser Ala Asp Asn Ser Ser Gly Leu
450 455 460

Ala Val Thr Thr Leu Ser Pro Ala Ile Ala Tyr Asp Thr His Ser Leu
465 470 475 480

Gly Thr Asn Gly Ile Gly Gly Asp Ser Thr Ser Asn Gly Phe Ser Ser
485 490 495

Asn Ser Ala Pro Glu Ser Thr Ser Lys His Lys Ser Pro Arg Arg Arg
500 505 510

Lys Lys Arg Val Thr Ile Lys Pro Val Arg Phe Gly Ile Phe Leu Leu
515 520 525

Cys Leu Ala Gly Ile Val Gly Gly Ala Thr Ala Leu Ile Ile Asn Arg
530 535 540

Thr Gly Asp Pro Leu Gly Gly Leu Leu Glu Asp Pro Leu Asp Val Phe
545 550 555 560

Leu Asp Gln Pro Ser Glu Phe Ile Pro Asp Glu Ala Thr Ser Arg Asn
565 570 575

Leu Ile Leu Ser Gln Pro Asn Phe Asn Gln Gln Val Gly Gln Met Val
580 585 590

Val Gln Gly Trp Leu Asp Ser Lys Lys Leu Ala Phe Gly Gln Asn Tyr

595

600

605

Asp Val Gly Ala Leu Gln Ser Val Leu Ala Pro Asn Leu Leu Ala Gln
610 615 620

Gln Arg Gly Arg Ala Gln Arg Asp Gln Ala Gln Lys Val Tyr His Gln
625 630 635 640

Tyr Glu His Lys Leu Gln Ile Leu Ala Tyr Gln Val Asn Pro Gln Asp
645 650 655

Pro Asn Arg Ala Thr Val Thr Ala Arg Val Glu Glu Ile Ser Gln Pro
660 665 670

Phe Thr Leu Gly Asn Gln Gln Gln Lys Gly Ser Ala Thr Lys Asp Asp
675 680 685

Leu Thr Val Arg Tyr Gln Leu Val Arg His Gln Gly Val Trp Lys Ile
690 695 700

Asp Gln Ile Gln Val Val Asn Gly Pro Arg
705 710

<210> 171

<211> 819

<212> PRT

<213> Arabidopsis thaliana

<400> 171

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Leu Gln Ile Ser Gly Leu Leu Val Val Arg Ser Glu Ser Gly Glu Phe
35 40 45

Phe Gly Ser Gly Leu Ser Leu Arg Arg Phe Gln Arg Glu Gly Arg Arg
50 55 60

Arg Leu Asn Ala Ala Gly Gly Gly Ile His Val Val Asp Asn Ala Pro
65 70 75 80

Ser Arg Thr Ser Ser Leu Ala Ala Ser Thr Ser Thr Ile Glu Leu Pro
85 90 95

Val Thr Cys Tyr Gln Leu Ile Gly Val Ser Glu Gln Ala Glu Lys Asp
100 105 110
Glu Val Val Lys Ser Val Ile Asn Leu Lys Lys Thr Asp Ala Glu Glu
115 120 125
Gly Tyr Thr Met Glu Ala Ala Ala Arg Gln Asp Leu Leu Met Asp
130 135 140
Val Arg Asp Lys Leu Leu Phe Glu Ser Glu Tyr Ala Gly Asn Leu Lys
145 150 155 160
Glu Lys Ile Ala Pro Lys Ser Pro Leu Arg Ile Pro Trp Ala Trp Leu
165 170 175
Pro Gly Ala Leu Cys Leu Leu Gln Glu Val Gly Gln Glu Lys Leu Val
180 185 190
Leu Asp Ile Gly Arg Ala Ala Leu Arg Asn Leu Asp Ser Lys Pro Tyr
195 200 205
Ile His Asp Ile Phe Leu Ser Met Ala Leu Ala Glu Cys Ala Ile Ala
210 215 220
Lys Ala Ala Phe Glu Val Asn Lys Val Ser Gln Gly Phe Glu Ala Leu
225 230 235 240
Ala Arg Ala Gln Ser Phe Leu Lys Ser Lys Val Thr Leu Gly Lys Leu
245 250 255
Ala Leu Leu Thr Gln Ile Glu Glu Ser Leu Glu Gly Leu Ala Pro Pro
260 265 270
Cys Thr Leu Asp Leu Leu Gly Leu Pro Arg Thr Pro Glu Asn Ala Glu
275 280 285
Arg Arg Arg Gly Ala Ile Ala Ala Leu Arg Glu Leu Leu Arg Gln Gly
290 295 300
Leu Ser Val Glu Ala Ser Cys Gln Ile Gln Asp Trp Pro Cys Phe Leu
305 310 315 320
Ser Gln Ala Ile Ser Arg Leu Leu Ala Thr Glu Ile Val Asp Leu Leu
325 330 335
Pro Trp Asp Asp Leu Ala Ile Thr Arg Lys Asn Lys Lys Ser Leu Glu
340 345 350

Ser His Asn Gln Arg Val Val Ile Asp Phe Asn Cys Phe Tyr Met Val
355 360 365

Leu Leu Gly His Ile Ala Val Gly Phe Ser Gly Lys Gln Asn Glu Thr
370 375 380

Ile Asn Lys Ala Lys Thr Ile Cys Glu Cys Leu Ile Ala Ser Glu Gly
385 390 395 400

Val Asp Leu Lys Phe Glu Glu Ala Phe Cys Ser Phe Leu Leu Lys Gln
405 410 415

Gly Ser Glu Ala Glu Ala Leu Glu Lys Leu Lys Gln Leu Glu Ser Asn
420 425 430

Ser Asp Ser Ala Val Arg Asn Ser Ile Leu Gly Lys Glu Ser Arg Ser
435 440 445

Thr Ser Ala Thr Pro Ser Leu Glu Ala Trp Leu Met Glu Ser Val Leu
450 455 460

Ala Asn Phe Pro Asp Thr Arg Gly Cys Ser Pro Ser Leu Ala Asn Phe
465 470 475 480

Phe Arg Ala Glu Lys Lys Tyr Pro Glu Asn Lys Lys Met Gly Ser Pro
485 490 495

Ser Ile Met Asn His Lys Thr Asn Gln Arg Pro Leu Ser Thr Thr Gln
500 505 510

Phe Val Asn Ser Ser Gln His Leu Tyr Thr Ala Val Glu Gln Leu Thr
515 520 525

Pro Thr Asp Leu Gln Ser Pro Val Val Ser Ala Lys Asn Asn Asp Glu
530 535 540

Thr Ser Ala Ser Met Pro Ser Val Gln Leu Lys Arg Asn Leu Gly Val
545 550 555 560

His Lys Asn Lys Ile Trp Asp Glu Trp Leu Ser Gln Ser Ser Leu Ile
565 570 575

Gly Arg Val Ser Val Val Ala Leu Leu Gly Cys Thr Val Phe Phe Ser
580 585 590

Leu Lys Leu Ser Gly Ile Arg Ser Gly Arg Leu Gln Ser Met Pro Ile

595

600

605

Ser Val Ser Ala Arg Pro His Ser Glu Ser Asp Ser Phe Leu Trp Lys
610 615 620

Thr Glu Ser Gly Asn Phe Arg Lys Asn Leu Asp Ser Val Asn Arg Asn
625 630 635 640

Gly Ile Val Gly Asn Ile Lys Val Leu Ile Asp Met Leu Lys Met His
645 650 655

Cys Gly Glu His Pro Asp Ala Leu Tyr Leu Lys Ser Ser Gly Gln Ser
660 665 670

Ala Thr Ser Leu Ser His Ser Ala Ser Glu Leu His Lys Arg Pro Met
675 680 685

Asp Thr Glu Glu Ala Glu Glu Leu Val Arg Gln Trp Glu Asn Val Lys
690 695 700

Ala Glu Ala Leu Gly Pro Thr His Gln Val Tyr Ser Leu Ser Glu Val
705 710 715 720

Leu Asp Glu Ser Met Leu Val Gln Trp Gln Thr Leu Ala Gln Thr Ala
725 730 735

Glu Ala Lys Ser Cys Tyr Trp Arg Phe Val Leu Leu His Leu Glu Val
740 745 750

Leu Gln Ala His Ile Phe Glu Asp Gly Ile Ala Gly Glu Ala Ala Glu
755 760 765

Ile Glu Ala Leu Leu Glu Glu Ala Ala Glu Leu Val Asp Glu Ser Gln
770 775 780

Pro Lys Asn Ala Lys Tyr Tyr Ser Thr Tyr Lys Ile Arg Tyr Ile Leu
785 790 795 800

Lys Lys Gln Glu Asp Gly Leu Trp Lys Phe Cys Gln Ser Asp Ile Gln
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Ile Gln Lys

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<211> 2857
<212> DNA

<213> *Arabidopsis thaliana*

<400> 172

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gccgggctgc	tctcaggaac	cttgattcaa	agccatatat	tcatgatata	ttcttatcta	780
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<212> PRT
<213> Arabidopsis thaliana
<400> 173

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Leu Gln Ile Ser Gly Leu Leu Val Val Arg Ser Glu Ser Gly Glu Phe
35          40          45

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Phe Gly Ser Gly Leu Ser Leu Arg Arg Phe Gln Arg Glu Gly Arg Arg
50          55          60

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Arg Leu Asn Ala Ala Gly Gly Gly Ile His Val Val Asp Asn Ala Pro
65          70          75          80

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Ser Arg Thr Ser Ser Leu Ala Ala Ser Thr Ser Thr Ile Glu Leu Pro
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 Val Thr Cys Tyr Gln Leu Ile Gly Val Ser Glu Gln Ala Glu Lys Asp
 100 105 110
 Glu Val Val Lys Ser Val Ile Asn Leu Lys Lys Thr Asp Ala Glu Glu
 115 120 125
 Gly Tyr Thr Met Glu Ala Ala Ala Ala Arg Gln Asp Leu Leu Met Asp
 130 135 140
 Val Arg Asp Lys Leu Leu Phe Glu Ser Glu Tyr Ala Gly Asn Leu Lys
 145 150 155 160
 Glu Lys Ile Ala Pro Lys Ser Pro Leu Arg Ile Pro Trp Ala Trp Leu
 165 170 175
 Pro Gly Ala Leu Cys Leu Leu Gln Glu Val Gly Gln Glu Lys Leu Val
 180 185 190
 Leu Asp Ile Gly Arg Ala Ala Leu Arg Asn Leu Asp Ser Lys Pro Tyr
 195 200 205
 Ile His Asp Ile Phe Leu Ser Met Ala Leu Ala Glu Cys Ala Ile Ala
 210 215 220
 Lys Ala Ala Phe Glu Val Asn Lys Val Ser Gln Gly Phe Glu Ala Leu
 225 230 235 240
 Ala Arg Ala Gln Ser Phe Leu Lys Ser Lys Val Thr Leu Gly Lys Leu
 245 250 255
 Ala Leu Leu Thr Gln Ile Glu Glu Ser Leu Glu Gly Leu Ala Pro Pro
 260 265 270
 Cys Thr Leu Asp Leu Leu Gly Leu Pro Arg Thr Pro Glu Asn Ala Glu
 275 280 285
 Arg Arg Arg Gly Ala Ile Ala Ala Leu Arg Glu Leu Leu Arg Gln Gly
 290 295 300
 Leu Ser Val Glu Ala Ser Cys Gln Ile Gln Asp Trp Pro Cys Phe Leu
 305 310 315 320
 Ser Gln Ala Ile Ser Arg Leu Leu Ala Thr Glu Ile Val Asp Leu Leu

325

330

335

Pro Trp Asp Asp Leu Ala Ile Thr Arg Lys Asn Lys Lys Ser Leu Glu
 340 345 350

Ser His Asn Gln Arg Val Val Ile Asp Phe Asn Cys Phe Tyr Met Val
 355 360 365

Leu Leu Gly His Ile Ala Val Gly Phe Ser Gly Lys Gln Asn Glu Thr
 370 375 380

Ile Asn Lys Ala Lys Thr Ile Cys Glu Cys Leu Ile Ala Ser Glu Gly
 385 390 395 400

Val Asp Leu Lys Phe Glu Glu Ala Phe Cys Ser Phe Leu Leu Lys Gln
 405 410 415

Gly Ser Glu Ala Glu Ala Leu Glu Lys Leu Lys Gln Leu Glu Ser Asn
 420 425 430

Ser Asp Ser Ala Val Arg Asn Ser Ile Leu Gly Lys Glu Ser Arg Ser
 435 440 445

Thr Ser Ala Thr Pro Ser Leu Glu Ala Trp Leu Met Glu Ser Val Leu
 450 455 460

Ala Asn Phe Pro Asp Thr Arg Gly Cys Ser Pro Ser Leu Ala Asn Phe
 465 470 475 480

Phe Arg Ala Glu Lys Lys Tyr Pro Glu Asn Lys Lys Met Gly Ser Pro
 485 490 495

Ser Ile Met Asn His Lys Thr Asn Gln Arg Pro Leu Ser Thr Thr Gln
 500 505 510

Phe Val Asn Ser Ser Gln His Leu Tyr Thr Ala Val Glu Gln Leu Thr
 515 520 525

Pro Thr Asp Leu Gln Ser Pro Val Val Ser Ala Lys Asn Asn Asp Glu
 530 535 540

Thr Ser Ala Ser Met Pro Ser Val Gln Leu Lys Arg Asn Leu Gly Val
 545 550 555 560

His Lys Asn Lys Ile Trp Asp Glu Trp Leu Ser Gln Ser Ser Leu Ile
 565 570 575

Gly Arg Val Ser Val Val Ala Leu Leu Gly Cys Thr Val Phe Phe Ser
580 585 590

Leu Lys Leu Ser Gly Ile Arg Ser Gly Arg Leu Gln Ser Met Pro Ile
595 600 605

Ser Val Ser Ala Arg Pro His Ser Glu Ser Asp Ser Phe Leu Trp Lys
610 615 620

Thr Glu Ser Gly Asn Phe Arg Lys Asn Leu Asp Ser Val Asn Arg Asn
625 630 635 640

Gly Ile Val Gly Asn Ile Lys Val Leu Ile Asp Met Leu Lys Met His
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Cys Gly Glu His Pro Asp Ala Leu Tyr Leu Lys Ser Ser Gly Gln Ser
660 665 670

Ala Thr Ser Leu Ser His Ser Ala Ser Glu Leu His Lys Arg Pro Met
675 680 685

Asp Thr Glu Glu Ala Glu Glu Leu Val Arg Gln Trp Glu Asn Val Lys
690 695 700

Ala Glu Ala Leu Gly Pro Thr His Gln Val Tyr Ser Leu Ser Glu Val
705 710 715 720

Leu Asp Glu Ser Met Leu Val Gln Trp Gln Thr Leu Ala Gln Thr Ala
725 730 735

Glu Ala Lys Ser Cys Tyr Trp Arg Phe Val Leu Leu His Leu Glu Val
740 745 750

Leu Gln Ala His Ile Phe Glu Asp Gly Ile Ala Gly Glu Ala Ala Glu
755 760 765

Ile Glu Ala Leu Leu Glu Glu Ala Ala Glu Leu Val Asp Glu Ser Gln
770 775 780

Pro Lys Asn Ala Lys Tyr Tyr Ser Thr Tyr Lys Ile Arg Tyr Ile Leu
785 790 795 800

Lys Lys Gln Glu Asp Gly Leu Trp Lys Phe Cys Gln Ser Asp Ile Gln
805 810 815

Ile Gln Lys

<210> 174
 <211> 491
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> misc feature
 <222> (22)..(22)
 <223> n is a, c, g, or t

<220>
 <221> misc feature
 <222> (451)..(451)
 <223> n is a, c, g, or t

<220>
 <221> misc feature
 <222> (471)..(471)
 <223> n is a, c, g, or t

<220>
 <221> misc feature
 <222> (483)..(484)
 <223> n is a, c, g, or t

<220>
 <221> misc feature
 <222> (487)..(487)
 <223> n is a, c, g, or t

<220>
 <221> misc feature
 <222> (489)..(490)
 <223> n is a, c, g, or t

<400> 174
 ggccgctcggc aaatactgca gnttgcaeat gatactctca caaaccagag ctcccgcacc 60
 gagtatgacc gcgcgctctc tgaggaccgt gacgcggcgc tcacactgga tgttgcttgg 120
 gacaagggtc cggtgtgtct atgtgccctt caggaggctg gggaggcaca ggcagtgtct 180
 gcaattggag agcacttact ggaggaccgc ccgccaagc ggttcaagca ggatgtggtg 240
 ctggcaatgg cgctcgctta tgtggacata tcaagggatg caatggcggc tagccctcca 300
 gatgtaatcc gctgctgtga ggtgcttgaa agggctctca agctcttgca ggaggatggg 360
 gcaatcaacc ttgcacctgg tctgctttca caaattgatg aaactctgga ggagatcaca 420
 cctcgttgtg ttttgagact tcttgccctt nctcttgatg aaaaacatca nattgaacgc 480
 cannaangnn t 491

<210> 175
 <211> 545
 <212> DNA
 <213> Gossypium arboreum

<220>
 <221> misc_feature
 <222> (528)..(528)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (536)..(536)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (540)..(540)
 <223> n is a, c, g, or t

<400> 175
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 tcaccgcctt gataaattgc cagaggttct ggatgggtcaa atgttgaaga catggacaga 120
 tcgtgcagcc gaaatcgctc agcttggttg ggtatatgaa tatagtctac tgaacatggc 180
 cattgacagt gttacccttt cactagatgg ccagcgagct gtagtcgaag ctactctgga 240
 agaatccacc tgcttgactg atgttcatca tccggagaac aatgcctcta atgtaaactc 300
 ctacaccacg agatatgaga tgtcttgctc caactcaggc tggaaaatca ctgaaggatc 360
 tgtctacaaa tcttaactat gatgtataaa gcataaaaag cctgaaagct ccaatgtggt 420
 taccagcttt gcctttttac gtagctatat ttgttatatt gtttgagaaa acaagagtta 480
 gcgtttttcca gtcattgcaag cagttcaaat taaaagaggc aatgcttntc atgganaacn 540
 aaatg 545

<210> 176
 <211> 420
 <212> DNA
 <213> Hordeum vulgare

<400> 176
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 tggcagagca tcaaattcaa ggccttggga tcagatcatt ctgttgcac attgcaagag 120
 gttcttgatg gcaacatgct gaaggatgg acagaccgag cagcagagat tgagcgcaaa 180
 ggctggttct gggactacac gctgttcaac gtggcgatcg acagcatcac cgtctcctg 240
 gacggacggc gggcgaccgt ggaggcgaca attgaggagg cgggtcagct caccgacgca 300
 accgacccca ggaacgatga tttgtacgac actaagtaca ccaccggta cgagatggcc 360
 ttcaccggac caggaggggtg gaagataacc gaaggcgag tcctcaagtc gtcatagggc 420

<210> 177
 <211> 606
 <212> DNA
 <213> Triticum aestivum

<400> 177
ctgcaaactct agcactatgt ttctctttat ctccaggatc tagcctagca ccaacaatcc 60
aaatacaaca caagaaaaat aaagctcttc gtcgatcaca tcagactaac gcaactatcg 120
gtcttccaaa ctaaaaaggg cctagactgc ctgcttattt acacaccccc aaaagaaaac 180
tggaaggaat taacaaactt aatgagggtta ccgcacacca actaccctaa gacgacttga 240
ggaccgcgcc ttccattatc ttccaccctc ctagtccggt gaaggtcac tcataccggg 300
tggtgtactt cgtgtcgtac gagtcgttgt tcttggggtc ggttgcgtcg atgagctggc 360
ctgcctcctc gatcgttgcc tccacggtcg ccgcgcgtcc gtccaggag accgtgatgc 420
tgtcgatcgc cacgtcagac agtgtgtagt ccagaacca gcctttgcgc ccgatctccg 480
ctgctcggtc cgtccatacc ttcagcatgt tgccatcaag aacctcttgc aatgattcca 540
cagaatgatc tgatcccaag gccttggttt tgatactctg ccacttgcca acaatatctt 600
ctgcca 606

<210> 178
<211> 563
<212> DNA
<213> *Gossypium arboreum*

<400> 178
tttttttttt tttttttttt tttttttttt ttttttttaa cttgcctctt ttaatttgaa 60
ctgcttgcct gactggaaaa ccctaactct tgttttctca aacaatttaa caaatatagc 120
tccttaaaaa ggcaaagctg gtaaccacat tggagctttc aggcttttta tgctttatac 180
atcatagtta aaattttagt acagatcctt cagtgatctt ccaacctgag ttggaacaaa 240
acatctcata tttcgtgggg taggagttta cattacaggc attgttctcc ggatgatgaa 300
cattactcaa gccggggggg tcttccaaaa taacttcgac tacagctcgc tggccattta 360
atgaaagggg aacactgtca atggccctgt tcagtcaact ttattcatat acccaaccca 420
gctgaccgat ttcggctgca ccaactgtcc atgttttcaa catttgacca tccaaaacct 480
ttggcaattt atcaaggggg ggatcaagtc caaacgcctc agatttaatg ttctgccact 540
tgccaacaat gccttttgca att 563

<210> 179
<211> 360
<212> DNA
<213> *Hordeum vulgare*

<400> 179
gatgagccca tacagattcc taaaatggat gcgaagctgg cagaagatat tgttcgcaag 60
tggcagagca tcaaatacaa ggccttggga tcagatcatt ctgttgcac attgcaagag 120
gttcttgatg gcaacatgct gaaggatgg acagaccgag cagcagagat tgagcgcaaa 180

ggctggttct	gggactacac	gctgttcaac	gtggcgatcg	acagcatcac	cgctctccctg	240
gacggacggc	gggcgaccgt	ggaggcgaca	attgaggagg	cggttcagct	caccgacgca	300
accgacccca	ggaacgatga	ttgttacgac	actaagtaca	ccacccggta	cgagatggcc	360

<210> 180
 <211> 300
 <212> DNA
 <213> *Hordeum vulgare*

<400> 180	
tgatggcaac	atgctgaagg tatggacaga ccgagcagca gagattgagc gcaaaggctg 60
gttctgggac	tacacgctgt tcaacgtggc gatcgacagc atcaccgtct ccctggacgg 120
acggcggggcg	accgtggagg cgacaattga ggaggcgggt cagctcaccg acgcaaccga 180
ccccaggaac	gatgatttgt acgacactaa gtacaccacc cggtacgaga tggccttcac 240
cggaccagga	gggtggaaga taaccgaagg cgcagtcctc aagtcgtcat agggcggttca 300

<210> 181
 <211> 549
 <212> DNA
 <213> *Triticum monococcum*

<400> 181	
tttttttttt	tttttttttt ttttttttca gcggcaaatt cagcactatg tttctcttat 60
ccccaaactca	aagatcttct aagctagcaa taatccgaaa acgacacagg gaaaaacaaa 120
gctcatcgct	gattgcacat cagactaacc aaactatctc caacttccaa actgagaagg 180
gcctagactg	cttatattaca caccaaaaag aacacgggag gaatcaatca acaaaggctc 240
actgcacacc	gaacgcccta tgacgacttg aggaccgcac cttctgttat cttccaccct 300
cctggtccag	tgaaggatcat ctcgtaccgg gtgggtgtact tagtgctgta caaatcggtg 360
ttcctggggg	cggttgcacg ggtaagctgg cctgcctcct caattgtcgc ctccacagtc 420
gcccgtcgtc	cgtccaggga gacggtgatg ctgtcaatcg ccacgtcgga cagcgtgtag 480
tcccagaacc	agcctttgcg ctcgatctct gctgctcggt ccctccatac cttcagcatg 540
ttgccatca	549

<210> 182
 <211> 573
 <212> DNA
 <213> *Hordeum vulgare*

<220>
 <221> misc_feature
 <222> (6)..(6)
 <223> n is a, c, g, or t

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<220>
<221> misc_feature
<222> (16)..(16)
<223> n is a, c, g, or t

<400> 182
gcgagnaagg acgagnatcg tcaagtcggc catcgagctg aggaaatcgg agatcgaaga      60
tgggtacacg gaggaggtgt ccacctgcag acaggctctg ctgctggacg tgagagacaa      120
gcttctcttt gaacaggagt acgcaggaag caccagggcc aagggtccgc ccagatcctc      180
tcttcatata ccctggagct ggttgccctgc tgccttgtgt gtcttgcagg aggttgggga      240
agagaagctg gtcttggaca ttggtcaggc agctctacga cgccctgatt ctaagccata      300
tgctcacgat gtacttcttg caatggcact agctgaatgc tccattgcaa aagctagctt      360
tgaaaaaagt aaagtatctc ttggctttga ggctctagca cgtgctcaat atcttttgag      420
gaaaaaacca tctttagaga agatgcctct tcttgagcag atcgaagaat cacttgaaga      480
gcttgcacca gcttgcactc tagaggtttt aagcctgccc cgtacacctg aaaattctga      540
acgcaggcgt ggtgctattg cagctctctg tga                                  573

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<210> 183
<211> 400
<212> DNA
<213> Beta vulgaris

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<400> 183
gcataacacg gcaagaagat gttgcagtta atggcttttg aaatgaggat gttacaatgg      60
agcttggccg tgataacact ttagattatg tgaatttagc cagttcaaat tttactgaag      120
ataatatcga gcaagaatcg gttactgaga agataaaaga tttaggtgtg aaggttatgt      180
gtgccggtgt ggtgattgga ctgacaactt tggctggcat gaaacttttg cctggcagaa      240
gtgggtctgc cattccacac aggcattctg gttctgctgt ggcttctgat gtctccagtg      300
tggggctctc agtaaatgaa actactgagg agaaagtacc aaaaatggat gcaagacttg      360
cagaagttct agttagaaga tggcagaacg ttaaatcaca                                400

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<210> 184
<211> 631
<212> DNA
<213> Prunus persica

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<220>
<221> misc_feature
<222> (21)..(21)
<223> n is a, c, g, or t

<400> 184
gcagttgcaa ttgctggggg ngattcacta cgtgaaaatt tcatgaacga ggccttcttg      60

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catatgactg cagctgagca ggttgattta tttgtagcta cccccagtaa tatccccgga	120
gaaagctttg aagtttatgg ggtggctctt gcgcttggtg ctcaagcctt tgttggtaaa	180
aaacctcatc acattcaaga tgctgaaaac ctattccaga aacttcagca gtctaaggta	240
acagctgtag gacattctct tgacaactat ataaccaaag aaagcagtga gatagacttt	300
gctttggaga ggggactctg ttcacttctt ctaggggacc ttgatgacag tcgttcgtgg	360
ttgggcctag acagtaatga ttcaccatat agaaatccat ctggtgtaga ctttgtcttg	420
gagaactcaa aggatgacga tgacaatgac aatgacaatg atcttcctgg actttgcaag	480
ctattggaga cgtgggtgat ggaggtggta ttccccaggt ttagagacac caaagacata	540
gagttcagac tgggagacta ctatgatgat cctacagtct tgagatactt agaaaggctg	600
gatggcacta atggttcacc cttagctgct g	631

<210> 185
 <211> 647
 <212> DNA
 <213> Helianthus annuus

<400> 185	
cagaaagagg tggttgatt gatgactttg gctggcttga aatttatacc gtcttaaaca	60
ggctctacta gtactactgc tcgtaaagaa gttgattcgg ctctggcttc agacgtcacc	120
aatgtggagg attctagggt tgaggatgct gaagacattc ctaaaatgga tgcaagatta	180
gccgaaggtc tagttcgtaa gtggcagagc ataaaatccc aagcccttgg acctgagcat	240
tgccactcaa aattatcata ggtattagat ggtgaaatgc acaagatctg gcttcaacgg	300
gcaaccgaaa ttgctcaacg tggttggttt tgggactaca cgcttttaaa cattaccatt	360
gacagtgtta ccgtttcact cgatgggagc ttagctgttg tggaagcaac ccttgaagag	420
tctgccaaagt tgattgattt gacccacccg gaaaacaatg actcctataa tttaacttac	480
accacacgtt atgagatgtc gtgtgccaaag tcatcatgga aaatcacaaa gggggctgct	540
ctcaaatcat aacagatgta attctttctc accttttctg tatttatctg ttattagatt	600
actcagcagt tgaatgatat gtttctccac catttcgatc atgagcg	647

<210> 186
 <211> 652
 <212> DNA
 <213> Helianthus annuus

<400> 186	
tgtggtggtt ggattgatga ctttggctgg cttgaaattt acaccgtcca aaagaggctc	60
tactagtact actgctcgta aagaagttga ttcggctctg gcttcagacg tcaccaatag	120
gattctaggg ttgaggatgc tgaagacatt cctaaaatgg atgcaagatt agccgagggg	180

ctagttcgta agtggcagag cataaaatcc caagcccttg gacctgagca ttgccactca	240
aaattatcag aggtattaga tggtgaaatg cacaagatct ggcttcaacg ggcaaccgaa	300
attgctcaac gtggttggtt ttgggactac acgcttttaa acattaccat tgacagtgtt	360
accgtctcac tcgatgggcg cttagctgtt gtggaagcaa cccttgaaga gtctgccaa	420
ttgattgatt tgacccaccc ggaaaacaat gactcctata atttaactta caccacacgt	480
tatgagatgt cgtgtgccaa gtcttcatgg aaaatcacia agggggctgt cctcaaata	540
taacagatgt aattctttct caccttttct gtatttaact gttattagat tactcagcag	600
ttgaatgata tgtttctcca ccatatcgat catgagtgtg tttggtgctg cc	652

<210> 187
 <211> 460
 <212> DNA
 <213> *Populus tremula*

<400> 187	
gactgaaaaa ataaaagatg ccagtatcaa aatatgtgtg ctggtgtggc aattggactg	60
ctgacttttag ctggcctgaa gtgttttctt cctaggactg gtccttcat tcgacagaaa	120
gaaattgggtt cggcaatggc atctgacacc atcaatttga attcagcagt agatgaacia	180
atttccgagg acttaccacg aatggatgca aggggtgcag aggatatagt tcgcaagtgg	240
caaaacatta aatctcaggc ttttggaaact gatcactgcc tggcaaaatt gccagaggtt	300
ttggatagtc agatgttgaa aatatggaca gatcgtgcgg ccgaaattgc acatcttggt	360
tgggtatacg agtatatgct gttggacctg actattgaca gtgtgactgt atctgtagat	420
ggcctaaatg ctgtagtaga agcaaacctc aaagagtcaa	460

<210> 188
 <211> 3933
 <212> DNA
 <213> *Chlamydomonas reinhardtii*

<400> 188	
atgaactcgg cggagcacgt ctctgttgcc gtggactatt accgaatgct gcacgttccc	60
cgcgtaagcc gccctgacgc cattcgcaag gcgtatgaga acctggtgaa gcaaccccc	120
gctgccgcgt actctgcgga caccctcttc gcacgcgcgg tgctactcaa ggcagccgcg	180
gagtcgctga ccgaccgga cctgcgccgc tcatatgacg ccaagctggc cgctggtcac	240
acagccctgc gcgtcagcca gcaggacct cccggagccc ttgtcgtgct gcaggaggtg	300
agccgtgctc tggcgaccgc tcaaccctt gcgaccgcta aaaccatcag cacatatagc	360
acatataaat tcccatgggt tctgtactac cgccacccc tctgaagggg gcgagtattc	420
attcttcacg catgagcgca gacttttacc ctatcaagtc ccgccctcgc ccgccttctc	480

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aagggcggtg	cgctcatgcg	cggtgtgctg	cgcgccgccg	ccaccgtggc	cgccgccaca	1140
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- - -	- aggtcgcagc	caacaccgcc	gtggcagcct	cccgcgcgca	gcgcctcagc	3000
	cggccagcac	cgccaccgcc	tcgtcatctt	cctctgccgc	ccgcggcgct	3060
	ccctgagcgc	tgccaccgcc	gccgcacacg	ccgcgcgcgc	ccagcaggcg	3120
	gtgccagcat	cgtcggtgct	gacgtgctgc	ccccacacgc	agtggccgcg	3180
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	ccaccagccg	cggcgccagc	gcggccgctc	gtgcgcccac	agcaccagcc	3360
	ggccccagca	cggcgccgcc	tctgctgcgc	agtcgcaccg	ggaggaggat	3420
	acggcgggcca	ggaggggggg	gtgccgcggc	gcatgagcga	ggcggacctg	3480
	tggcgggcct	ggagaaggcc	atgtgggact	cggagctgcc	gccgccgccg	3540
	cgcagaaggc	gctcacctac	gccgcaggac	tggtaggttg	ctgcgcagcc	3600
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	ttaggacatg	aattgcatca	acgctgcaaa	tctggtgtat	ggtacgcgcg	3720
	ccaacaaggc	tggtgaccaa	gctgctgctg	cccttgact	ctttcaacgc	3780
	ctggccgtgg	tggtagcctt	cctggtgtcc	agcttcttcc	gccgcaacga	3840
	tccgccctgg	caccgcgcgc	cgtcaccacc	gcctccgtgg	ccgttagcgc	3900
	aagccgggca	aggccaccgc	ctccgcgcac	tga		3933

<210> 189

<211> 2511

<212> DNA

<213> Chlamydomonas reinhardtii

<400> 189

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cccgcgcgcg gcgacgtggc cgctgccgtg gccctggcct actgtgaccg cgctggtgag	420
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accgccgccc ggcgcgcca gggcgtggcg ctcatgcgcg gtgtgctgcg cgccgccgcc	720
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<210> 190
 <211> 836
 <212> PRT
 <213> Chlamydomonas reinhardtii
 <400> 190

Met Asn Ser Ala Glu His Val Ser Val Ala Val Asp Tyr Tyr Arg Met
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Leu His Val Pro Arg Val Ser Arg Pro Asp Ala Ile Arg Lys Ala Tyr
 20 25 30

Glu Asn Leu Val Lys Gln Pro Pro Ala Ala Ala Tyr Ser Ala Asp Thr
 35 40 45

Leu Phe Ala Arg Ala Val Leu Leu Lys Ala Ala Ala Glu Ser Leu Thr
 50 55 60

Asp Pro Asp Leu Arg Arg Ser Tyr Asp Ala Lys Leu Ala Ala Gly His
 65 70 75 80

Thr Ala Leu Arg Val Ser Gln Gln Asp Leu Pro Gly Ala Leu Val Val
 85 90 95

Leu Gln Glu Ile Gly Glu His Gln Leu Val Leu Asp Leu Gly Leu Arg
 100 105 110

Trp Leu Glu Val Asn Gly Gly Gln Pro Asp Ala Gly Asp Val Ala Ala
 115 120 125

Ala Val Ala Leu Ala Tyr Cys Asp Arg Ala Gly Glu Arg Leu Thr Ser
 130 135 140

Gln Leu Gln Pro Pro Pro Ala Ser Ala Leu Pro Gly Pro Asp Gly Ala
 145 150 155 160
 Ala Val Pro His Ala His Val Gly Ala Val Leu Pro Ala Cys Asp Asp
 165 170 175
 Leu Asp Ala Ala Leu Ser Lys Leu Arg Arg Tyr Gly Met Ala Gln Gln
 180 185 190
 Leu Gln Gln Gln Ile Val Gly Ala Leu Arg Asp Leu Ala Pro Glu Tyr
 195 200 205
 Ala Cys Glu Leu Ala Ala Leu Pro Leu Gly Ala Glu Thr Ala Ala Arg
 210 215 220
 Arg Ala Lys Gly Val Ala Leu Met Arg Gly Val Leu Arg Ala Ala Ala
 225 230 235 240
 Thr Val Ala Ala Ala Thr Ala Lys Pro Glu Ala Ala Ala Asp Asp Ser
 245 250 255
 Asp Asp Asp Glu Val Asp Pro Arg Ser Val Leu Ala Ala Ala Arg Arg
 260 265 270
 Met Leu Thr Arg Ser Arg Asp Val Leu Thr Cys Ser Glu Gln Val Ala
 275 280 285
 Leu Leu Pro Asp Ala Leu Arg Gly Ser Gly Val Ser Pro Thr Pro Asp
 290 295 300
 Ala Leu Tyr Asp Gly Ala Leu Ala His Leu Val Asp Gly Phe Arg Asn
 305 310 315 320
 Gly Trp Pro His Ser Val His Gln Ala Asp Gln Leu Leu Ala Lys Leu
 325 330 335
 Glu Ala Gln Gln Ala Arg Ala Ala Ala Met Arg Arg Glu Gln Ser Glu
 340 345 350
 Leu Ala Ala Ala Ala Ala Ala Arg Arg Ala Met Tyr Ser Gly Pro Ala
 355 360 365
 Ala Ala His Gly Pro Thr Leu Tyr Thr Asn Tyr Asn Asn Pro Ala Gly
 370 375 380
 Ser Gly Asn Gly Ala Pro Pro Pro Pro Pro Arg Pro Met Pro Met Val

385		390		395		400
Pro	Arg	Gly	Asp	Gly	Gln	His
			405			
				Ala	Met	Ala
				410		
				Ala	Ala	Ser
					Val	Ala
						415
Val	His	Ser	Thr	Ala	Met	Ala
			420			
				Glu	His	Ala
				425		
				Ala	Ala	Arg
					Ser	Ala
						430
Gly	Ala	Ala	Gly	Ala	Ser	Asp
				440		
				Gly	Gly	Ala
						His
					Ala	Asn
						445
					Gly	Val
						Ala
Leu	Glu	Arg	Ala	Val	Cys	Ala
						455
				Val	Leu	Leu
					Gly	Asp
						460
					Tyr	Thr
						Ala
						Ala
Val	Glu	Arg	Leu	Gly	Leu	Asp
						470
				Thr	Asn	Ala
						475
				Ala	Ala	Val
					Glu	Gln
						480
Leu	Arg	Glu	Phe	Val	Leu	Ala
						485
				Ala	His	Ser
						490
				Pro	Asn	Gly
					Arg	Gly
						495
Arg	Pro	Gly	Leu	Arg	Ala	Leu
						500
				Ala	Leu	Ala
						505
				Thr	Arg	Trp
					Leu	Glu
						510
					Gly	Val
						Ala
Leu	Ala	Ser	Phe	Arg	Asp	Thr
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				Ala	Gly	Ser
						520
				Pro	Val	Pro
						525
				Pro	Pro	Leu
						Glu
Ala	Ser	Trp	Phe	Ala	Asp	Leu
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				Ala	Arg	Val
						535
				Ala	Phe	Tyr
						540
				Leu	Gln	Val
						Trp
Arg	Leu	Cys	Arg	Val	Glu	Gln
						545
				Val	Leu	Ala
						550
				Ala	Ala	Ala
						555
				His	Phe	Leu
						560
Asn	Leu	Leu	Pro	Asn	Met	Leu
						565
				Lys	Ala	Ile
						570
				Ala	Gly	Thr
						575
Val	Ala	Ala	Asn	Thr	Ala	Val
						580
				Ala	Ala	Ser
						585
				Arg	Ala	Gln
						590
				Arg	Leu	Ser
Ala	Thr	Val	Ala	Ala	Ser	Thr
						595
				Ala	Thr	Ala
						600
				Ser	Ser	Ser
						605
				Ser	Ser	Ser
						610
				Ala	Thr	Ala
						615
				Ala	Leu	Ser
						620
				Ala	Thr	Ala
						625
				Ala	Thr	Ala
						630
				Ala	Asn	Ala
						635
				Val	Gly	Ala
						640
				Ser	Ile	Val

Gly Ala Asp Val Leu Pro Pro Thr Ala Val Ala Ala Ala Ala Ala Ala
645 650 655

Gly Thr Ala Ala Ala Ala Val Thr Gly Pro Ala Leu Gly Arg Gly
660 665 670

Ala Ala Ala Ser Ala Ser Ser Phe Glu Glu Gly Ala Ala Glu Ala Ala
675 680 685

Asp Leu Arg Arg Arg Phe Val Ala Thr Ser Arg Gly Ala Ser Ala Ala
690 695 700

Val Gly Ala Pro Thr Ala Pro Ala Ala Met Thr Gly Pro Gln His Gly
705 710 715 720

Ala Ala Ser Ala Ala Gln Ser His Arg Glu Glu Asp Glu Asp Ser His
725 730 735

Gly Gly Gln Glu Gly Gly Val Pro Arg Arg Met Ser Glu Ala Asp Leu
740 745 750

Arg Ala His Leu Ala Gly Leu Glu Lys Ala Met Trp Asp Ser Glu Leu
755 760 765

Pro Pro Pro Pro Pro Ser Arg Ala Gln Lys Ala Leu Thr Tyr Ala Ala
770 775 780

Gly Leu Leu Ala Val Val Val Ala Phe Leu Val Ser Ser Phe Phe Arg
785 790 795 800

Arg Asn Asp Gly Ala Ala Ser Ala Leu Ala Pro Ala Ala Val Thr Thr
805 810 815

Ala Ser Val Ala Val Ser Ala Gln Pro Ala Lys Pro Gly Lys Ala Thr
820 825 830

Arg Ser Ala His
835

<210> 191
<211> 2022
<212> DNA
<213> Thermosynechococcus elongatus

<400> 191
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accacagttg	ccacccgtcg	cgaactcatt	gagcaggcct	atgcagtttt	gcgagaaccg	180
gagcagcgcg	atgcctacga	tcgccactgc	cgtaccgttg	atccccgatga	tttgattgcc	240
cagttggatc	ccgatgccac	cactccccac	attgaaatta	gtgatgagca	attgtcgggg	300
gcactcctac	tgctgtatga	actaggaaat	tatgcccaag	ttgtcaacct	gggagacgcc	360
tttcttaaaa	aggatgtttt	tgagcgcaat	cgccccata	cttcccctgc	cgccgttgcc	420
gacattaccc	tcactgtggc	tttggcctat	ctggaattgg	gacgggagga	atggcagcgg	480
cagtcctatg	aatcagccgc	ctctcagcta	gaagccggtc	tccaggtact	tcagcgggta	540
aatttgtttc	ccgagctcca	ggagcagttt	cagacggaac	tgaatcggct	gcgtccctac	600
cgcattctgg	aattactggc	actgcctttg	tccgatagtg	cgaatcggca	gcgggggtatt	660
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tcaggactaa	cagttgagga	ttttctgaaa	tttatTTTTgc	aactgcgcag	ccatcttacc	780
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gacgtgtgg	aggtgttggc	agaagtcaac	gaggatgccc	gtttctatga	acaggggaacc	1920
ctgcgcactg	atatttcccta	tagcgatccc	taccgggtca	tttatacctt	tatccgtcgc	1980

ggcaatcaat gggtgattca aggcattgcag gtgggttagtt aa

2022

<210> 192
<211> 673
<212> PRT
<213> Thermosynechococcus elongatus

<400> 192

Met Arg Ile Pro Leu Asp Tyr Tyr Gln Val Leu Gly Val Pro Ile Gln
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Ala Thr Pro Glu Gln Ile Glu Gln Ala Phe Arg Asp Arg Leu Leu Gln
20 25 30

Leu Pro Thr His Gln His Ser Pro Thr Thr Val Ala Thr Arg Arg Glu
35 40 45

Leu Ile Glu Gln Ala Tyr Ala Val Leu Arg Glu Pro Glu Gln Arg Asp
50 55 60

Ala Tyr Asp Arg His Cys Arg Thr Val Asp Pro Asp Asp Leu Ile Ala
65 70 75 80

Gln Leu Asp Pro Asp Ala Thr Thr Pro His Ile Glu Ile Ser Asp Glu
85 90 95

Gln Leu Ser Gly Ala Leu Leu Leu Leu Tyr Glu Leu Gly Asn Tyr Ala
100 105 110

Gln Val Val Asn Leu Gly Asp Ala Phe Leu Lys Lys Asp Val Phe Glu
115 120 125

Arg Asn Arg Pro Tyr Thr Ser Pro Ala Ala Val Ala Asp Ile Thr Leu
130 135 140

Thr Val Ala Leu Ala Tyr Leu Glu Leu Gly Arg Glu Glu Trp Gln Arg
145 150 155 160

Gln Ser Tyr Glu Ser Ala Ala Ser Gln Leu Glu Ala Gly Leu Gln Val
165 170 175

Leu Gln Arg Val Asn Leu Phe Pro Glu Leu Gln Glu Gln Phe Gln Thr
180 185 190

Glu Leu Asn Arg Leu Arg Pro Tyr Arg Ile Leu Glu Leu Leu Ala Leu
195 200 205

Pro Leu Ser Asp Ser Ala Asn Arg Gln Arg Gly Ile Leu Leu Leu Arg
 210 215 220
 Gln Met Leu Ser Glu Arg Gly Gly Ile Glu Gly Arg Gly Asp Asp Arg
 225 230 235 240
 Ser Gly Leu Thr Val Glu Asp Phe Leu Lys Phe Ile Leu Gln Leu Arg
 245 250 255
 Ser His Leu Thr Val Ala Glu Gln Gln Glu Leu Phe Glu Arg Glu Ser
 260 265 270
 Arg Arg Pro Ser Ala Val Ala Thr Tyr Leu Ala Val His Ala Leu Val
 275 280 285
 Ala Arg Gly Val His Glu Leu Gln Pro Ser Tyr Ile Cys Arg Ala Lys
 290 295 300
 Asp Leu Leu Gln Gln Leu Leu Pro His Gln Asp Val Tyr Leu Glu Leu
 305 310 315 320
 Ala Ser Cys Leu Leu Leu Leu Gly Gln Pro Thr Glu Ala Leu Ala Ala
 325 330 335
 Leu Asp His Ser Gln Asp Gln Pro Thr Leu Asp Phe Ile Arg Arg His
 340 345 350
 Ala Gly Glu Ala Gly Asp Arg Leu Pro Gly Leu Tyr Tyr Tyr Thr Thr
 355 360 365
 Gln Trp Leu Thr Glu Glu Ile Tyr Pro Ala Phe Arg Asp Leu Gly Glu
 370 375 380
 Thr Pro Val Ala Leu Glu Ala Tyr Phe Ala Asp Ala Asn Val Gln Thr
 385 390 395 400
 Tyr Leu Glu Ala Leu Ser Glu Asp Ser Ile Ala Pro Glu Pro Pro Ala
 405 410 415
 Thr Thr Ala Ser Ala Leu Pro Glu Val Ile Arg Pro Thr Val Ala Val
 420 425 430
 Pro Pro Pro Leu Ser Phe Thr Ala Glu Thr Leu Pro Leu Gln Asp Gln
 435 440 445
 Ser Arg Leu Gly Gln Gly Leu Ser Ala Ser Ala Phe Thr Pro Ser Ala
 450 455 460

Thr Ala Thr Gly Thr Ser Met Pro Gln Pro Ser Pro Arg Lys Arg Arg
465 470 475 480

Ser Pro Arg Asn Arg Cys Ala Gln Lys Arg Gln Thr Trp Phe Trp Met
485 490 495

Gly Ala Gly Val Val Leu Val Gly Leu Gly Ala Leu Ala Lys Val Tyr
500 505 510

Trp Pro Ala Lys Thr Ala Glu Ala Pro Pro Pro Pro Val Thr Pro Ala
515 520 525

Pro Thr Pro Val Ala Thr Pro Thr Pro Thr Pro Gln Pro Thr Thr Leu
530 535 540

Ala Ile Thr Leu Thr Pro Glu Met Ala Arg Asp Arg Leu His Thr Trp
545 550 555 560

Gln Gln Ile Lys Ala Gln Ala Leu Gly Arg Pro Phe Glu Val Asp Lys
565 570 575

Leu Thr Thr Ile Leu Ala Glu Pro Glu Leu Ser Arg Trp Arg Ser Arg
580 585 590

Ala Gln Gly Leu Lys Ser Glu Gly Ser Tyr Trp Val Tyr Thr Leu Lys
595 600 605

Asn Leu Glu Val Lys Glu Val Arg Leu Gln Arg Ser Asp Arg Val Glu
610 615 620

Val Leu Ala Glu Val Asn Glu Asp Ala Arg Phe Tyr Glu Gln Gly Thr
625 630 635 640

Leu Arg Thr Asp Ile Ser Tyr Ser Asp Pro Tyr Arg Val Ile Tyr Thr
645 650 655

Phe Ile Arg Arg Gly Asn Gln Trp Leu Ile Gln Gly Met Gln Val Val
660 665 670

Ser

<210> 193

<211> 2370

<212> DNA

<213> Trichodesmium erythraeum

<400> 193

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gccacaatag ttgctcgtaa acagcttata gatgaggctt atgctgttct ttgcgatcct	180
gaacaacgtc aaacctatga tggtaacttt ttagctaaaa cctacgagcc aatagtagaa	240
gaactcaatc caagttctca gataaatttt gatcaagcac aagaaaaaga aaccacactt	300
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tatcaaaaaca gagagactaa agctgcctct gatttttcatt ctaatacccc tagtatagaa	420
atagaatatc cacaatttgt gggagccatc ctaattttac atgagctagg agaatatgag	480
ctagtattaa aaataactca cccttatctt cttaacaata gtataactat taaagatgga	540
cgttttggag acccagcatt agttttgcca gatgttgctc ttacagttgc tctagcaaat	600
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gaagcccttc gcccttccgc agttggtgca tatctagcgg ttatacttt tttagctcaa	1020
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gaaaattctc aacaatctcc agattttattg ccagggtctat gtctctatgc tgaacattgg	1260
ttgacagagg aggtttttcc acatttccgt gatttgctcg acaagtcagc ttctttgaaa	1320
gattattttg cagatcaaca tgttcaagct tatctagaag ctttacctac agaagcagag	1380
gtagctaatc aatgggtagt cgttcagcct cgtcgtagta atcacaataa aaaacaaatg	1440
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ggtcgtttaa tattaatcgc aattgtggga tttttgttaa taggatttat tgggttggtta	1860

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 aatactaaca atgaaaactt atttggtcgt tatgatttag ttcgtaaaag tcaaaaatgg 2340
 caaattagta attggaaggt attgagataa 2370

<210> 194
 <211> 789
 <212> PRT
 <213> Trichodesmium erythraeum

<400> 194

Val Arg Ile Pro Leu Asp Tyr Tyr Arg Ile Leu Gly Leu Pro Ile Gln
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Ala Thr Ala Glu Gln Leu Arg Gln Ala His Gln Asp Arg Thr Gln Gln
 20 25 30

Phe Pro Arg Arg Glu Tyr Ser Glu Ala Thr Ile Val Ala Arg Lys Gln
 35 40 45

Leu Ile Asp Glu Ala Tyr Ala Val Leu Cys Asp Pro Glu Gln Arg Gln
 50 55 60

Thr Tyr Asp Gly Asn Phe Leu Ala Lys Thr Tyr Glu Pro Ile Val Glu
 65 70 75 80

Glu Leu Asn Pro Ser Ser Gln Ile Asn Phe Asp Gln Ala Gln Glu Lys
 85 90 95

Glu Thr Thr Leu Lys Glu Thr Arg Glu Val Leu Pro Glu Ile Ala Ser
 100 105 110

Lys Gln Leu Lys Lys Arg Thr Ser Tyr Gln Asn Arg Glu Thr Lys Ala
 115 120 125

Ala Ser Asp Phe His Ser Asn Thr Pro Ser Ile Glu Ile Glu Tyr Pro
 130 135 140

Gln Phe Val Gly Ala Ile Leu Ile Leu His Glu Leu Gly Glu Tyr Glu
145 150 155 160

Leu Val Leu Lys Ile Thr His Pro Tyr Leu Leu Asn Asn Ser Ile Thr
165 170 175

Ile Lys Asp Gly Arg Phe Gly Asp Pro Ala Leu Val Leu Pro Asp Val
180 185 190

Val Leu Thr Val Ala Leu Ala Asn Leu Glu Leu Gly Arg Glu Glu Trp
195 200 205

Gln Gln Gly Gln Tyr Glu Ser Ala Ala Thr Ala Leu Glu Ala Gly Leu
210 215 220

Gly Leu Leu Leu Arg Glu Asn Leu Phe Val Gln Ile Arg Gly Glu Ile
225 230 235 240

Gln Ala Asp Leu Tyr Lys Leu Arg Pro Tyr Arg Ile Met Glu Leu Ile
245 250 255

Ala Leu Pro Glu Glu Ile Ala Leu Asp Arg Ser Arg Gly Leu Glu Ile
260 265 270

Leu Gln Asp Met Leu Asn Glu Arg Gly Gly Ile Asp Gly Gln Gly Glu
275 280 285

Asp Ser Ser Gly Leu Gly Ile Glu Asp Phe Leu Lys Phe Val Gln Gln
290 295 300

Leu Arg Gln Tyr Leu Thr Thr Ala Glu Gln Lys Lys Leu Phe Glu Ala
305 310 315 320

Glu Ala Leu Arg Pro Ser Ala Val Gly Ala Tyr Leu Ala Val Tyr Thr
325 330 335

Phe Leu Ala Gln Gly Phe Ala Gln Lys Gln Pro Ala Phe Ile Arg Lys
340 345 350

Ala Lys Leu Met Leu Met Gln Leu Gly Arg Ser Gln Asp Val Asn Leu
355 360 365

Glu Lys Ser Val Cys Ala Leu Leu Leu Gly Gln Thr Glu Glu Ala Ser
370 375 380

Arg Ser Leu Glu Leu Ser His Glu Asn Glu Pro Leu Ser Phe Ile Lys
385 390 395 400

Glu Asn Ser Gln Gln Ser Pro Asp Leu Leu Pro Gly Leu Cys Leu Tyr
 405 410 415
 Ala Glu His Trp Leu Thr Glu Glu Val Phe Pro His Phe Arg Asp Leu
 420 425 430
 Ser Asp Lys Ser Ala Ser Leu Lys Asp Tyr Phe Ala Asp Gln His Val
 435 440 445
 Gln Ala Tyr Leu Glu Ala Leu Pro Thr Glu Ala Glu Val Ala Asn Gln
 450 455 460
 Trp Val Val Val Gln Pro Arg Arg Ser Asn His Asn Lys Lys Gln Met
 465 470 475 480
 Phe Asp Pro Lys Glu Leu Glu Lys Leu Asn Val Ser Asp Leu Glu Asp
 485 490 495
 Lys Asp Ile Ser Arg Val Asp Ala Thr Ala Thr Gly Ile Val Ala Ser
 500 505 510
 Gly Ser Gln Gly Ser Ser Asn Leu Leu Gly Ala Ser Ser Asp Gly Leu
 515 520 525
 Leu Gln Glu Leu Glu Lys Ser Ser Ser Thr Arg Gly Gly Pro Lys Gln
 530 535 540
 Val Thr Thr Lys Ser Ser Ser His Tyr Leu Gly Lys Ile Arg Glu Lys
 545 550 555 560
 Ser Ile Ser Gly Leu Pro Glu Phe Asn Glu Ser Thr Ser Ile Glu Ser
 565 570 575
 Gly Gly Leu Pro Gln Ser Ile Gln Glu His Ser Ser Arg Arg Thr Ser
 580 585 590
 Ala Arg Arg Glu Pro Val Lys Phe Gly Arg Leu Ile Leu Ile Ala Ile
 595 600 605
 Val Gly Phe Leu Leu Ile Gly Phe Ile Gly Leu Leu Thr Ile Lys Thr
 610 615 620
 Ile Gly Trp Leu Val Asn Ala Leu Gly Trp Glu Arg Glu Lys Leu Met
 625 630 635 640
 Ile Gln Leu Asp Arg Pro Pro Ile Glu Ile Pro Glu Pro Asp Arg Val

645					650					655					
Asn	Leu	Ala	Ala	Ser	Gly	Pro	Ile	Thr	Lys	Glu	Val	Ala	Arg	Arg	Thr
		660						665					670		
Ile	Gln	Ser	Trp	Leu	Asp	Ile	Lys	Ala	Ser	Ala	Leu	Gly	Pro	Asn	His
		675					680					685			
Lys	Ile	Glu	Gln	Leu	Pro	Asn	Ile	Leu	Val	Glu	Pro	Ala	Leu	Ser	Arg
	690					695					700				
Trp	Leu	Pro	Thr	Ala	Asn	Ala	Leu	Lys	Gln	Glu	Lys	Ser	Tyr	Arg	Arg
705					710					715					720
Tyr	Glu	His	Asp	Leu	Glu	Ile	Ser	Asn	Ile	Lys	Met	Ser	Asn	Thr	Asn
				725					730					735	
Ser	Asn	Leu	Ala	Gln	Val	Asp	Ala	Lys	Val	Ile	Glu	Lys	Val	Glu	Phe
			740					745					750		
Tyr	Ser	Asp	Asn	Gly	Arg	Leu	Thr	Asn	Thr	Asn	Asn	Glu	Asn	Leu	Phe
		755					760					765			
Val	Arg	Tyr	Asp	Leu	Val	Arg	Lys	Ser	Gln	Lys	Trp	Gln	Ile	Ser	Asn
	770					775					780				
Trp	Lys	Val	Leu	Arg											
785															
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<211>	765														
<212>	PRT														
<213>	Homo sapiens														
<400>	195														
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Gln	Asp	Ala	Phe	Ser	Ala	Ile	Gly	Gln	Asn	Ala	Asp	Leu	Asp	Leu	Pro
		20					25					30			
Gln	Ile	Ala	Val	Val	Gly	Gly	Gln	Ser	Ala	Gly	Lys	Ser	Ser	Val	Leu
	35					40					45				
Glu	Asn	Phe	Val	Gly	Arg	Val	Thr	Arg	Arg	Pro	Leu	Val	Leu	Gln	Leu
	50					55					60				

Val Asn Ala Thr Thr Glu Tyr Ala Glu Phe Leu His Cys Lys Gly Lys
65 70 75 80

Lys Phe Thr Glu Ala Glu Thr Asp Arg Val Thr Gly Thr Asn Lys Gly
85 90 95

Ile Ser Pro Val Pro Ile Asn Leu Arg Val Tyr Ser Pro His Val Leu
100 105 110

Asn Leu Thr Leu Val Asp Leu Pro Gly Met Thr Lys Val Pro Val Gly
115 120 125

Asp Gln Pro Pro Asp Ile Glu Phe Gln Ile Arg Asp Met Leu Met Gln
130 135 140

Phe Val Thr Lys Glu Asn Cys Ser Asp Leu Ala Asn Ser Asp Ala Leu
145 150 155 160

Lys Val Ala Lys Glu Val Asp Pro Gln Gly Gln Arg Thr Ile Gly Val
165 170 175

Ile Thr Lys Leu Asp Leu Met Asp Glu Gly Thr Asp Ala Arg Asp Val
180 185 190

Leu Glu Asn Lys Leu Leu Pro Leu Arg Arg Gly Tyr Ile Gly Val Val
195 200 205

Asn Arg Ser Gln Lys Asp Ile Asp Gly Lys Lys Asp Ile Thr Phe Leu
210 215 220

Ser His Pro Ser Tyr Arg His Leu Ala Asp Arg Met Gly Thr Pro Tyr
225 230 235 240

Leu Gln Lys Val Leu Asn Gln Gln Leu Thr Asn His Ile Arg Asp Thr
245 250 255

Leu Pro Gly Leu Arg Asn Lys Leu Gln Ser Gln Leu Leu Ser Ile Glu
260 265 270

Lys Glu Val Glu Glu Tyr Lys Asn Phe Arg Pro Asp Asp Pro Ala Arg
275 280 285

Lys Thr Lys Ala Leu Asp Phe Glu Lys Arg Ile Glu Gly Ser Gly Asp
290 295 300

Gln Ile Asp Thr Tyr Glu Leu Ser Gly Gly Ala Arg Ile Asn Arg Ile
305 310 315 320

Phe His Glu Arg Phe Pro Phe Glu Leu Val Lys Met Glu Phe Asp Glu
325 330 335
Lys Glu Leu Arg Arg Glu Ile Ser Tyr Ala Ile Lys Asn Ile His Gly
340 345 350
Ile Arg Thr Gly Leu Phe Thr Pro Asp Met Ala Lys Lys Ile Arg Glu
355 360 365
Pro Cys Leu Lys Cys Val Asp Met Val Ile Ser Glu Leu Ile Ser Thr
370 375 380
Val Arg Gln Cys Thr Lys Lys Leu Gln Gln Tyr Pro Arg Leu Arg Glu
385 390 395 400
Glu Met Glu Arg Ile Val Thr Thr His Ile Arg Glu Arg Glu Gly Arg
405 410 415
Thr Lys Glu Gln Val Met Met Asn Thr Asn His Glu Asp Phe Ile Gly
420 425 430
Phe Ala Asn Ala Gln Gln Arg Ser Asn Gln Met Asn Lys Lys Lys Thr
435 440 445
Ser Gly Asn Gln Asp Glu Ile Leu Val Ile Arg Lys Gly Trp Leu Thr
450 455 460
Ile Asn Asn Ile Gly Ile Met Lys Gly Gly Ser Lys Glu Tyr Trp Phe
465 470 475 480
Val Leu Thr Ala Glu Asn Leu Ser Trp Tyr Lys Asp Asp Ser Val Asp
485 490 495
Asn Leu Lys Leu Arg Asp Val Glu Lys Gly Phe Met Ser Ser Lys His
500 505 510
Ile Phe Ala Leu Phe Asn Thr Glu Gln Arg Asn Val Tyr Lys Asp Tyr
515 520 525
Arg Gln Leu Glu Leu Ala Cys Glu Thr Gln Glu Glu Val Asp Ser Trp
530 535 540
Lys Ala Ser Phe Leu Arg Ala Gly Val Tyr Pro Glu Arg Val Gly Asp
545 550 555 560
Lys Glu Lys Asp Ser Phe Met His Ser Met Asp Pro Gln Leu Glu Arg

Val Met Tyr Asp Ser Gly Ile Asp Thr Leu Asp Leu Pro Ile Leu Ala
20 25 30

Val Val Gly Ser Gln Ser Ser Gly Lys Ser Ser Ile Leu Glu Thr Leu
35 40 45

Val Gly Arg Val Thr Arg Arg Pro Leu Val Leu Gln Leu Asn Asn Ile
50 55 60

Ser Pro Asn Ser Pro Leu Ile Glu Glu Asp Asp Asn Ser Val Asn Pro
65 70 75 80

His Asp Glu Val Thr Lys Ile Ser Gly Phe Glu Ala Gly Thr Lys Pro
85 90 95

Leu Glu Tyr Arg Gly Lys Glu Arg Asn His Ala Asp Glu Trp Gly Glu
100 105 110

Phe Leu His Ile Pro Gly Lys Arg Phe Tyr Glu Asn Glu Thr Ala Arg
115 120 125

Ile Ala Gly Lys Asp Lys Gly Ile Ser Lys Ile Pro Ile Asn Leu Lys
130 135 140

Val Phe Ser Pro His Val Leu Asn Leu Thr Leu Val Asp Leu Pro Gly
145 150 155 160

Ile Thr Lys Val Pro Ile Gly Glu Gln Pro Pro Asp Ile Glu Lys Gln
165 170 175

Ile Lys Asn Leu Ile Leu Asp Tyr Ile Ala Thr Pro Asn Cys Val Asp
180 185 190

Leu Val Asn Ser Glu Ser Leu Lys Leu Ala Arg Glu Val Asp Pro Gln
195 200 205

Gly Lys Arg Thr Ile Gly Val Ile Thr Lys Leu Asp Leu Met Asp Ser
210 215 220

Gly Thr Asn Ala Leu Asp Ile Leu Ser Gly Lys Met Tyr Pro Leu Lys
225 230 235 240

Leu Gly Phe Val Gly Val Val Asn Arg Ser Gln Gln Asp Ile Gln Leu
245 250 255

Asn Lys Thr Val Glu Phe Arg Lys His Pro Val Tyr Arg Thr Ile Ser
260 265 270

Thr Lys Cys Gly Thr Arg Tyr Leu Ala Lys Leu Leu Asn Gln Thr Leu
 275 280 285
 Leu Ser His Ile Arg Asp Lys Leu Pro Asp Ile Lys Thr Lys Leu Asn
 290 295 300
 Thr Leu Ile Ser Gln Thr Glu Gln Glu Leu Ala Arg Tyr Gly Gly Val
 305 310 315 320
 Gly Ala Thr Thr Asn Glu Ser Arg Ala Ser Leu Val Asn Phe Ile Ser
 325 330 335
 Ser Ile Asp Gly Thr Ser Ser Asp Ile Asn Thr Lys Glu Leu Cys Gly
 340 345 350
 Gly Ala Arg Ile Tyr Tyr Ile Tyr Asn Asn Val Phe Gly Asn Ser Leu
 355 360 365
 Lys Ser Ile Asp Pro Thr Ser Asn Leu Ser Val Leu Asp Val Arg Thr
 370 375 380
 Ala Ile Arg Asn Ser Thr Gly Pro Arg Pro Thr Leu Phe Val Pro Glu
 385 390 395 400
 Leu Ala Lys Leu Leu Leu Glu Pro Ser Gln Arg Cys Val Glu Leu Val
 405 410 415
 Tyr Glu Glu Leu Met Lys Ile Cys His Lys Cys Gly Ser Ala Glu Leu
 420 425 430
 Ala Arg Tyr Pro Lys Leu Lys Ser Met Leu Ile Glu Val Ile Ser Glu
 435 440 445
 Leu Leu Arg Glu Arg Leu Gln Pro Thr Arg Ser Tyr Val Glu Ile Asn
 450 455 460
 Thr Asn His Pro Asn Phe Leu Ser Ala Thr Glu Ala Met Asp Asp Ile
 465 470 475 480
 Met Lys Thr Arg Arg Lys Arg Asn Gln Glu Leu Leu Lys Ser Lys Leu
 485 490 495
 Ser Gln Gln Glu Asn Gly Gln Thr Asn Gly Ile Asn Gly Thr Ser Ser
 500 505 510
 Ile Ser Ser Asn Ile Asp Gln Asp Asp Gly Ile Asp Ala Glu Ser Lys

515	520	525
Gln Thr Lys Asp Lys Phe Leu Asn Tyr Phe Phe Gly Lys Asp Lys Lys 530 535 540		
Gly Gln Pro Val Phe Asp Ala Ser Asp Lys Lys Arg Ser Ile Ala Gly 545 550 555 560		
Asp Gly Asn Ile Glu Asp Phe Arg Asn Leu Gln Ile Ser Asp Phe Ser 565 570 575		
Leu Gly Asp Ile Asp Asp Pro Leu Thr Glu Arg Glu Glu Leu Glu Cys 580 585 590		
Glu Leu Ile Lys Arg Leu Ile Val Ser Tyr Phe Asp Ile Ile Arg Glu 595 600 605		
Met Ile Glu Asp Gln Val Pro Lys Ala Val Met Cys Leu Leu Val Asn 610 615 620		
Tyr Cys Lys Asp Ser Val Gln Asn Arg Leu Val Thr Lys Leu Tyr Lys 625 630 635 640		
Glu Thr Leu Phe Glu Glu Leu Leu Arg Glu Leu Cys Val Lys Ser Leu 645 650 655		
Gly Val Tyr Lys Lys Ala Ala Thr Leu Ile Ser Asn Ile Leu 660 665 670		
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Glu Asp Asp Ala Ala Ile Glu Glu Arg Trp Ser Leu Tyr Glu Ala Tyr 20 25 30		
Asn Glu Leu His Ala Leu Ala Gln Glu Leu Glu Thr Pro Phe Glu Ala 35 40 45		
Pro Ala Val Leu Val Val Gly Gln Gln Thr Asp Gly Lys Ser Ala Leu 50 55 60		

Val Glu Ala Leu Met Gly Phe Lys Thr Arg Arg Pro Ile Thr Leu His
65 70 75 80

Met Lys Tyr Asp Pro Gln Cys Gln Phe Pro Leu Cys His Leu Gly Ser
85 90 95

Asp Asp Asp Pro Ser Val Ser Leu Pro Lys Glu Ala Glu Asn Met Arg
100 105 110

Leu Glu Gln Glu Pro Cys Ser Pro Phe Ser Ala Lys Glu Ile Ile Val
115 120 125

Lys Val Gln Tyr Lys Tyr Cys Pro Asn Leu Thr Ile Ile Asp Thr Pro
130 135 140

Gly Leu Ile Ala Pro Ala Pro Gly Leu Lys Asn Arg Ala Leu Gln Val
145 150 155 160

Gln Ala Arg Ala Val Glu Ala Leu Val Arg Ala Lys Met Gln His Lys
165 170 175

Glu Ser Asp Trp Ser Ile Ala Thr Thr Arg Arg Ile Val Met Gln Val
180 185 190

Asp Pro Glu Leu Ser Arg Thr Ile Val Val Ser Thr Lys Leu Asp Thr
195 200 205

Lys Ile Pro Gln Phe Ser Cys Ser Ser Asp Val Glu Val Phe Leu Ser
210 215 220

Pro Pro Ala Ser Ala Leu Asp Ser Ser Leu Leu Gly Asp Ser Pro Phe
225 230 235 240

Phe Tyr Gly Gln Asp Ser Val Tyr Lys Ser Asn Asp Glu Phe Lys Gln
245 250 255

Ala Val Ser Leu Arg Glu Met Glu Asp Ile Ala Ser Leu Glu Lys Lys
260 265 270

Leu Gly Arg Leu Leu Thr Lys Gln Glu Lys Ser Arg Ile Gly Ile Ser
275 280 285

Lys Leu Arg Leu Phe Leu Glu Glu Leu Leu Trp Lys Arg Tyr Lys Glu
290 295 300

Ser Val Pro Leu Ile Ile Pro Leu Arg Lys Leu Asp Thr Val Ser Lys
305 310 315 320

Glu Leu Ser Ser Leu Asp Glu Ala Lys Leu Lys Glu Arg Gly Arg Thr
325 330 335

Phe His Asp Leu Phe Leu Thr Lys Leu Ser Leu Leu Leu Lys Gly Thr
340 345 350

Val Val Ala Pro Pro Asp Lys Phe Gly Glu Thr Leu Gln Asp Glu Arg
355 360 365

Thr Gln Gly Gly Ala Phe Val Gly Thr Asp Gly Leu Gln Phe Ser Arg
370 375 380

Leu Tyr Gly Gly Ala Gln Tyr His Arg Ala Met Ala Glu Phe Arg Phe
385 390 395 400

Leu Val Gly Ala Ile Lys Cys Pro Pro Ile Thr Arg Glu Glu Ile Val
405 410 415

Asn Ala Cys Gly Val Glu Asp Ile His Asp Gly Thr Asn Tyr Ser Arg
420 425 430

Thr Ala Cys Val Ile Ala Val Ala Lys Ala Arg Glu Thr Phe Glu Pro
435 440 445

Phe Leu His Gln Leu Gly Leu Leu Pro Ile Ser Val Tyr Leu Leu Gln
450 455 460

Lys Glu Gly Glu Tyr Leu Ser Gly His Glu Val Phe Leu Lys Arg Val
465 470 475 480

Ala Ser Ala Phe Asn Ser Phe Val Glu Ser Thr Glu Lys Ser Cys Arg
485 490 495

Asp Lys Cys Met Glu Asp Leu Ala Ser Thr Thr Arg Tyr Val Thr Trp
500 505 510

Ser Leu His Asn Lys Asn Ser Phe Gly Gly Thr Glu His Asn Thr Thr
515 520 525

Ser Gly Asn Ala Ile Gly Phe Ser Leu Pro Gln Asp Ala Leu Gly Gly
530 535 540

Thr Thr Asp Thr Lys Ser Arg Ser Asp Val Lys Leu Ser His Leu Ala
545 550 555 560

Ser Asn Ile Asp Ser Gly Ser Ser Ile Gln Thr Thr Glu Met Arg Leu

565

570

575

Ala Asp Leu Leu Asp Ser Thr Leu Trp Asn Arg Lys Leu Ile Val Tyr
580 585 590

Ala Leu Val Gln Gln Ile Phe Gln Gly Ile Arg Glu Tyr Phe Leu Ala
595 600 605

Ser Ala Glu Leu Lys Phe Asn Cys Phe Leu Leu Met Pro Ile Val Asp
610 615 620

Lys Leu Pro Ala Leu Leu Arg Glu Glu Leu Glu Asn Ala Phe Glu Asp
625 630 635 640

Asp Leu Asp Ser Ile Phe Asp Ile Thr Asn Leu Arg Thr Glu Ile Glu
645 650 655

Leu Arg Arg Val Lys Arg Ile Lys Glu Lys Phe Arg Val Met Asn Glu
660 665 670

Lys Leu Asn Ser His Glu Phe Ala Gln Asn Leu Lys Ala Pro Ser Val
675 680 685

Gln His
690

<210> 198
<211> 712
<212> DNA
<213> Lactuca sativa

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<221> misc feature
<222> (608)..(608)
<223> n is a, c, g, or t

<220>
<221> misc feature
<222> (656)..(656)
<223> n is a, c, g, or t

<400> 198
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aagggaccag gtgacataac ggggtggtgct tattagatct tccatgcatt tttcatggca 120
tgatctttcg gtggattcag caaagttata gaaagcagat gaaacacgtc tcaagaaaac 180
ttcatggcca cttaggaatt cgccttcttt ctgaagaaga taaacggaga tgggaagtaa 240
tctcttgaga atgtgaagaa gtcgactgcc caactgatga agaaaagggtt caaaagtatc 300

acgagctttt gcaacagcga tgacacatgc agtcctggag taatttggtc catcatgaat	360
atcttcgacc ccacatgcat tcacaatttc ttcacgtgta attgcagggc attttatccc	420
tccaacaaca aacctaaatt cagccatggc acgatgatat tgtgcacctc catatagacg	480
catacctgca ttaggtatta gtttgtgtgg gaactgagag ccatcaatac cgattaatgc	540
ccctccatta accctctcat cttgtagtgt ttccccaat ttatctggag gtgcaacaac	600
tgtccctntt catagcagtg ataacttggg aaggaaaaga tcatgaaaag atctcncttt	660
ctcctttagt ttgacttcat ctaaagtgtc gagttcttga tttatgtcat tt	712

<210> 199
 <211> 666
 <212> DNA
 <213> *Medicago truncatula*

<220>
 <221> misc feature
 <222> (646)..(646)
 <223> n is a, c, g, or t

<400> 199	
atctaaagta acaaccacca caaaacacaa caatggagga agaaagagaa caccaccaac	60
tcaaagacaa agaagaaaac gagtggcggtc tctacgaagc ttacaatgaa cttcacgcgc	120
ttgctcaaga acttcacacg ctttcgacg cgccggcggt actggttgtg ggccaccaaa	180
cagacgggaa gagcgctta gttgaggctc taatgggctt ccagttcaac cacgtcgggtg	240
gtggcaccaa aaccgcgcg cccattactc ttcacatgaa atatggccca cattgcgagt	300
ctccttcttg ctatcttctt tctgatgatg acccttctct ttctcaccat atgtcacttt	360
cccaaatcca gggttatatt gaagctgaga atgcgagggt ggagcgtgac tcatgttgtc	420
aattttcagc taaggaaata atcataaaag tggaatacaa atactgtccc aatctcacca	480
taatagacac accaggatta gttgctcctg caccaggctg taaaaatagg gcgatacagg	540
cacaggcacg agcggtagag tcaactggtc gtgcaaaaat gcagcacaag gagttcatta	600
tactctgtct tgaagattgt agtgattgga gcaatgcgac tacgangcgc gttgtaatgc	660
aaattg	666

<210> 200
 <211> 663
 <212> DNA
 <213> *Medicago truncatula*

<400> 200	
gtctttatgg ggggtgcacaa tatcatcgag caatggctga atttcgtttt gtagttggag	60
gaatcaagtg ccctccaatt acccggaag aaattgtaaa tgcttgtgga gttgaagaca	120

ttcatgatgg aacaaactac tctaggactg cttgtgtaat tgctgttgca aaggctcatg	180
atacatttga accttttctt catcagttgg ggtctagatt gttgcacata cttaagagat	240
tgctcccaat ctctttttat cttcttcaga aagattgtga gtatctaagt ggccatcagg	300
tgttcctcag gcgtgttgcc tccgccttcg acaactttgc agaatccact gaaaaatcat	360
gccgtgaaaa atgtatggag gacttggtaa gcaccacacg atatgtctca tggctcttac	420
acaataagag tcgggcagga ttacgccagt tcttagattc atttggtgga acagaacatt	480
ccaatgtttg taatgatccc actgcaactg ttctatcaca aacaaatgtg caagagaagg	540
aagacacaaa gccacaacta gaagtaaagc tcagtcacgt ggcctctgga actgataccta	600
gcacatccac ccagacagct gaaacaaagc ttgctgacct tcttgatagt acactttgga	660
atc	663

<210> 201
 <211> 622
 <212> DNA
 <213> *Prunus persica*

<220>
 <221> misc_feature
 <222> (609)..(609)
 <223> n is a, c, g, or t

<400> 201	
gcttataacct aacgcaggaa tgcgtttata tgggtggtgca caataccacc gtgccatggc	60
tgagttccgc tttgtagttg gaggaataaa atgccctcca attacaaggg aagaaattgt	120
aaatgcatgt ggagttgaag atttacatga tggcacaaac tactcaagga cagcttgtgt	180
aatagccgtt gcaaaggccc gtgatacatt tgagcctttc cttcatcagt taggtttag	240
actcttgcac attctaaaga gattacttcc tatatcagtc tatcttcttc agaaagatgg	300
tgagtattta agtggccatg aggtgtttct taggcgtggt gcttctgctt tcaatgactt	360
tgcagaatct accgaaaggg catgtcgtga aaaatgcatg gaggatttag taagcaccac	420
ccgctatgtc acctggtccc ttcacaacaa gaatcgagct gggttacgtc aatttttaga	480
ctcgttcgct ggaacagAAC ataacactat gggtagtaat tgcgtacctg ctggtatttc	540
ccaagattca tcctttgggt ctgttgccaa tgagaaggat actaagtcaa gggcagatgt	600
gaagctcanc catgtggcgt ct	622

<210> 202
 <211> 752
 <212> DNA
 <213> *Solanum tuberosum*
 <400> 202

gcgaatgtga ttcttcaaag gcaacaaagg ctgacggagg aatttgtgcc tcgtgcagat	60
ctgcttctgt ttctcatgtc tgctgatcga ccattaactg aaagtgaggt tagttttctg	120
cgttacactc agcagtggag taagaaggtc atttttgtgc tgaacaagtc tgacatatac	180
aagaataacg gcgagttgga ggaggccatt gcatttatca aagaaaatac acggaaattg	240
ctgaatacag aatccgtaac actgtatcca gtatctgcac ggctcgctct tgaatcaaag	300
ctttctactt ttgatgggtgc ccttagtcaa aacaatggga gttcaaataa tgattctcac	360
tggaaaacca agagcttcta tgagcttgag aagtacttgt ctagcttttt ggattcatcc	420
acaagtactg gaattgagag aatgaagctg aagcttgaaa ctccaattgc cattgcagaa	480
caactacttt tagcttgtca aggacttgtg agacaagaat gtcagcaagc caaacaagac	540
ttgctgtttg ttgaggatct tgtcaacagc gtagaagagt gcacaaagaa gctggaagtt	600
gatagcattc tgtggaagag gcaggttcta tctctgataa actctgctca agcacgtgtt	660
gtccggcttg tagagtcaac gttacaactg tcaaagtgtg atcttgtcgc tacatatgta	720
ttcagaagag aaaactctac tcaaagtcca gc	752

<210> 203
 <211> 492
 <212> DNA
 <213> Glycine max

<400> 203	
tggtgaatga agctattgaa gctatcaaga gggctgcacc tctgatggag gaggtttcac	60
ttcttaatga tgcgggtttct caaattgatg agccattctt actgggtata gtgggggaat	120
tcaactctgg taaatctacc gtgattaatg cgcttcttgg agaaagatat ctcaaagagg	180
gagttgttcc aacaactaat gagatcacat ttttacgata tactgactta gatattgaac	240
aacaacggtg tgaaaggcat ccagatggcc aatatatttg ctacattcct gctccaattc	300
ttaaagagat gaccattgtt gatacacctg gaactaatgt gattcttcag aggcagcagc	360
gtcttacaga ggaatttgta ccccgtcag atttacttct ttttgtcatt tctgctgac	420
gccctttaac tggaagtgag attgcttttc ttcgttattc tcagcagtgg aaaaagaaag	480
cggtctttgt ct	492

<210> 204
 <211> 446
 <212> DNA
 <213> Lycopersicon esculentum

<400> 204	
gagaccatta agtacaattc tataagcagt cttttgaaaa aagatggact tcattggtga	60
atccgtctga ccaaattgag ttaggaacaa ctggtgtgct ggatagaaaa tctgaagtta	120

ccataagtgt catagaggat ttcagtgtg cagctgcttc aaaattgctt gagagagata 180
 ttcgtgaagt gttcttgggt acttttgggt gtcttggagc agctgggtta tcagcgtcgc 240
 ttctgacatc tgttcttcaa accacattag aagacctcct tgcacttggc ctttgttctg 300
 ctggcggggtt attagcggtc ttcaacttct catcccgagg acagcaagtg gtagataaag 360
 taaagaggac tgctgatggc ctttcacgtg aactcgaaga ggctatgcag aaggagctct 420
 tggagacgac tagtaatgtg gaggac 446

<210> 205
 <211> 521
 <212> DNA
 <213> *Populus balsamifera* subsp. *trichocarpa*

<400> 205
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 ttctcgaact gaatcagttg ttctaccttt ggtagccagg attgtgcaga caccatatgc 120
 tgcattaaat gcgtctaatt ctgaagggtgc tgattttctt atatatgttc atggcccaga 180
 ggatgatcct gatgtagaaa tgagccctgg attcgggaat gtgaagatac caatctttgt 240
 cctcaatgct tcacgtgggg aggacacatt gtcggtgggg gcatcaaaat ttctgaaaac 300
 cggtgctagt ggtttagttc tgtcattgga agatttgagg ttatttagcg atgatgcttt 360
 gagtcagatg tttgacactc tgagtgaac cggtaaaaac tttcaggatg accttgaaag 420
 cttcagtaag ctcaaata tggatatgga aaatgatatt catgaaaaaa caacggtggc 480
 aggctttgtt aaactggagg atagagaaaa acagctcata g 521

<210> 206
 <211> 324
 <212> PRT
 <213> *Arabidopsis thaliana*

<400> 206

Met Glu Ala Leu Ser His Val Gly Ile Gly Leu Ser Pro Phe Gln Leu
 1 5 10 15

Cys Arg Leu Pro Pro Ala Thr Thr Lys Leu Arg Arg Ser His Asn Thr
 20 25 30

Ser Thr Thr Ile Cys Ser Ala Ser Lys Trp Ala Asp Arg Leu Leu Ser
 35 40 45

Asp Phe Asn Phe Thr Ser Asp Ser Ser Ser Ser Ser Phe Ala Thr Ala
 50 55 60

Thr Thr Thr Ala Thr Leu Val Ser Leu Pro Pro Ser Ile Asp Arg Pro

65		70		75		80
Glu Arg His Val	Pro 85	Ile Pro Ile Asp	Phe 90	Tyr Gln Val	Leu Gly 95	Ala
Gln Thr His	Phe 100	Leu Thr Asp Gly	Ile 105	Arg Arg Ala	Phe Glu 110	Ala Arg
Val Ser Lys	Pro 115	Pro Gln Phe Gly	Phe 120	Ser Asp Asp	Ala Leu 125	Ile Ser
Arg Arg Gln	Ile Leu 130	Gln Ala Ala Cys	Glu Thr 140	Leu Ser Asn	Pro Arg	
Ser Arg Arg	Glu Tyr 145	Asn Glu Gly	Leu Leu 155	Asp Asp Glu	Glu Ala 160	Thr
Val Ile Thr	Asp Val 165	Pro Trp Asp	Lys Val 170	Pro Gly Ala	Leu Cys 175	Val
Leu Gln Glu	Gly Gly 180	Glu Thr Glu	Ile Val 185	Leu Arg Val	Gly Glu 190	Ala
Leu Leu Lys	Glu Arg 195	Leu Pro Lys	Ser Phe 200	Lys Gln Asp	Val Val 205	Leu
Val Met Ala	Leu Ala 210	Phe Leu Asp	Val Ser 215	Arg Asp Ala	Met Ala 220	Leu
Asp Pro Pro	Asp Phe 225	Ile Thr Gly	Tyr Glu 230	Phe Val Glu	Glu Ala 235	Leu 240
Lys Leu Leu	Gln Glu 245	Glu Gly Ala	Ser Ser 250	Leu Ala Pro	Asp Leu 255	Arg
Ala Gln Ile	Asp Glu 260	Thr Leu Glu	Glu Ile 265	Thr Pro Arg	Tyr Val 270	Leu
Glu Leu Leu	Gly Leu 275	Pro Leu Gly	Asp Asp 280	Tyr Ala Ala	Lys Arg 285	Leu
Asn Gly Leu	Ser Gly 290	Val Arg Asn	Ile Leu 295	Trp Ser Val	Gly Gly 300	Gly
Gly Ala Ser	Ala Leu 305	Val Gly Gly	Leu Thr 310	Arg Glu Lys	Phe Met 315	Asn 320

Glu Ala Phe Leu ,